

(a) incubating a biological sample from said subject, which is suspected of containing an NTP, in the presence of a binding molecule capable of identifying an NTP; and

5 (b) detecting molecule which is bound in the sample, wherein the detection indicates that the subject has a glioblastoma.

The invention additionally includes the methods as above, wherein a biological sample is removed a human subject prior to contacting the sample with the molecule.

10 The invention additionally includes the methods as above, wherein detecting any of the molecules bound to the protein is performed by *in situ* imaging.

The invention additionally includes the methods as above, wherein detecting of any of the molecule bound to the protein is performed by *in vivo* imaging.

15 The invention additionally includes the methods as above, wherein the biological sample is reacted with the binding molecule in a manner and under such conditions sufficient to determine the presence and the distribution of the protein.

20 The invention additionally includes the methods as above, wherein a detectably labeled binding molecule of an NTP is administered to a human subject.

The invention additionally includes the methods as above, wherein the binding molecule is bound to the protein *in vivo*.

25 The invention additionally involves an NTP substantially free of any natural impurities and having a molecular weight of about 42 kDa.

The invention additionally involves an NTP substantially free of any natural impurities and having a molecular weight of about 26 kDa.

The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 21 kDa.

The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 17 kDa.

The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 14 kDa.

5       The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 8 kDa.

10       The present invention also particularly relates to the diagnostic methods recited above, wherein the immunoassay comprises two different antibodies bound to a solid phase support combined with a third different detectably labeled antibody in solution.

The invention is also directed to a method of producing an NTP, said method comprising:

- (a)     culturing a recombinant host comprising a human gene coding for said NTP; and
- 15       (b)     isolating said NTP from said host.

Additionally, the invention is directed to a substantially pure NTP obtained by the such a process.

20       The invention is also directed to an 15- to 30-mer antisense oligonucleotide which is complementary to an NTP nucleic acid sequence and which is nonhomologous to PTP nucleic acid sequences, as well as pharmaceutical compositions comprising such oligonucleotides and a pharmaceutically acceptable carrier.

25       The invention is also directed to ribozymes comprising a target sequence which is complementary to an NTP sequence and nonhomologous to PTP nucleic acid sequences, as well as pharmaceutical compositions comprising such ribozymes and a pharmaceutically acceptable carrier.

The invention is also directed to a method of achieving pharmaceutical delivery of NTP molecules to the brain through acceptable carriers or expression vectors.

30       The invention is also directed to oligodeoxynucleotides that form triple stranded regions with the various NTP genes (nucleic acid sequences) and

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which are nonhomologous to PTP nucleic acid sequences, as well as pharmaceutical compositions comprising such oligodeoxynucleotides and a pharmaceutically acceptable carrier.

5 The invention is also directed to the therapeutic use of NTP-derived molecules or fragments thereof to modify or improve dementias of the Alzheimer's type of neuronal degeneration.

The invention is also directed to methods for the differential diagnosis of sporadic and familial Alzheimer's disease.

### *Brief Description of the Drawings*

10 Figure 1 (panels A-J) shows neural thread protein immunoreactivity in CNS-derived tumors.

Figure 2 depicts a graph showing neural thread protein levels in PNET1, PNET2, A172, C6, and Huh7 hepatocellular carcinoma cells measured by a forward sandwich monoclonal antibody-based  
15 immunoradiometric assay (M-IRMA).

Figure 3 shows molecular size of neural thread proteins in SH-Sy5y, A172, and C6 cells demonstrated by immunoprecipitation and Western blot analysis using the Th9 monoclonal antibody.

20 Figure 4 shows molecular sizes of neural thread proteins in PNET1 cells (a) and C6 glioblastoma cells (b) demonstrated by pulse-chase metabolic labeling with <sup>35</sup>S-methionine, and immunoprecipitation with Th9 monoclonal antibody (left panel). The molecular weights are 8, 14, 17, 21, 26 and 42 kDa (arrows).

25 Figure 5 depicts a series of five graphs showing the 21 kDa and 17 kDa neural thread proteins in SH-Sy5y, PNET1, A172, and C6 cells and the absence thereof in Huh7 cells by SDS-PAGE/M-IRMA.

Figure 6 depicts a gel showing that the 21 kDa neural thread protein in C6 glioblastoma cells is phosphorylated.

Figure 7 depicts a bar graph showing altered neural thread protein expression in PNET1 cells with growth phase.

Figure 8 (panels A-F) shows altered phenotype of PNET1 cells with cessation of cell growth and overnight serum starvation.

5 Figure 9 shows the 1-9a partial cDNA sequence, and Figure 9a shows a partial sequence of the second 5' anchor PCR product corresponding to the 5' region of the 1-9a cDNA (WP5' Sequence).

10 Figure 10 shows alignment of partial sequences between 1-9a and human PTP and the Reg gene (the nucleic acid sequence corresponding to the genomic clone of human PTP).

Figure 10a shows alignment between 1-9a and Exon 2 of the human Reg gene, and between the first 5' anchor PCR product of 1-9a (WP03-417) and Exon 2 and Reg.

15 Figure 10b shows alignment between the 1-9a and its second 5' anchor PCR product (WP5') and AD 3-4 and AD 2-2 cDNAs.

Figure 11 shows the partial nucleic acid and deduced amino acid sequences of the HB4 cDNA as well as a protein hydrophilicity window plot.

Figure 11a shows alignment between HB4 and human PTP.

Figure 11b shows alignment between HB4 and human Reg gene.

20 Figure 12 (panels A-C) shows the expression of mRNA molecules corresponding to the 1-9a CNS neural thread protein cDNA sequence in neuroectodermal tumor cell lines and in rat pancreas.

25 Figure 13 (panels A and B) shows mRNA transcripts corresponding to the 1-9a CNS neural thread protein cDNA sequence in human brain. This figure also demonstrates higher levels of 1-9a CNS neural thread protein-related mRNAs in AD brains compared with aged-matched controls (panel A). Panel B demonstrates four different transcripts with greater abundance of the lower molecular size mRNAs in AD compared with aged controls.

30 Figure 14 (panels A-C) shows 1-9a Southern blot analysis of RT/PCR-derived cDNAs in neuroectodermal cell lines. A- and B-PCR amplification of 1-9a mRNA sequences in neuroectodermal cell lines, and using mRNA

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from newborn rat (NB) brain, AD brain, and aged control brain. Panel A is a longer exposure of Panel B. Panel C shows hybridization of the same blot using the O18 rat PTP probe.

Figure 15 (panels A and B) (SE-RT/PCR) shows hybridization of the 1-9a and O18 probes with several clones isolated from SH-Sy5y cells by reverse transcribing mRNA and amplifying with primers corresponding to the known sequence of the 1-9a partial cDNA.

Figures 16, 16a and 16b show the partial nucleic acid sequences of the AD 2-2 cDNAs isolated from the AD brain library. Figure 16 also shows a hydrophilicity window plot of AD2-2 T7.

Figures 16c, 16d, 16e and 16f show the partial nucleic acid sequences of the AD 3-4 cDNAs isolated from the AD brain library. Figure 16c also shows a hydrophilicity window plot of AD3-4.

Figures 16g, 16h and 16i show the partial nucleic acid sequences of the AD 4-4 cDNAs isolated from the AD brain library.

Figure 16j shows the partial nucleic acid sequences of the AD 16c (also called AD 10-7) cDNAs isolated from the AD brain library. Figure 16j also shows a hydrophilicity window plot of AD16c-T7.

Figure 16k shows the complete nucleotide sequence of the AD10-7 cDNA clone that was isolated from an AD library.

Figure 16l shows the complete nucleotide sequence of the AD16c cDNA clone that was isolated from the AD brain library.

Figure 17 shows alignment of partial sequences between AD 2-2 and human Reg gene.

Figure 17a shows alignment of partial sequences between AD 2-2 and Exon 1 of Reg and rat PTP.

Figure 17b shows alignment of partial sequences between AD 2-2 and 1-9a.

Figure 17c shows alignment of partial sequences between AD 2-2 and AD 16c.

Figure 18 shows alignment of partial sequences between AD 3-4 (also called AD 5-3) and the Reg gene.

Figure 18a shows alignment of partial sequences between AD 3-4 and the 5' anchor PCR products of the 1-9a mRNA, termed WPO3-5 and 18-4.

Figure 18b shows alignment of partial sequences between AD 3-4 and the G2a-a *EcoRI/PstI* genomic clone.

Figure 19 shows alignment of partial sequences between AD 4-4 and AD 2-2 and 1-9a (also called SE-4 corresponding to the PCR clone which is identical to 1-9a).

Figure 20 shows alignment of partial sequences between AD 16c and Reg gene.

Figure 20a shows alignment of partial sequences between AD 16c and human PTP.

Figure 20b shows alignment of partial sequences between AD 16c and AD 2-2.

Figure 21 (panel A) shows a genomic Southern blot analysis using the AD 3-4 as a probe; Figure 21 (panel B) shows a similar pattern of hybridization on a genomic Southern using AD 2-2 as a probe. Figure 21 (panel C) shows a Northern blot analysis of neuroectodermal tumor cell lines using AD 3-4 as a probe. The four cell lines that exhibit AD 3-4 transcripts are neuronal in phenotype; C6 glioma cell mRNA did not hybridize with the AD 3-4 probe. Figure 21 (panel D) shows a Northern analysis of human AD and aged control brain temporal lobe tissue using the AD 3-4 probe, and demonstrates over-expression of the corresponding gene in AD (lanes labeled A) compared with aged control brains (lanes labeled C).

Figures 22, 22a, 22b, 22c, 22d, 22e, 22f, 22g and 22h shows partial sequences of four genomic clones (isolated using both the 1-9a cDNA and rat PTP O-18 cDNA as probes).

Figures 23 and 23a show the alignment of the G2a-2 *PstI* partial sequence with the Reg gene.

Figure 23b shows alignment of the G2a-2 *Pst*I-*Eco*RI sequence and the Reg gene and the rat PTP.

Figures 23c and 23d show the alignment of the G5d-1 *Pst*I sequence and the Reg gene.

5 Figure 24 shows neural thread protein expression by the 1-9a cDNA (panel A) and the G2a-2 *Pst*I genomic clone (panel B). Panels C and D show negative expression by the G5d-1 *Eco*RI/*Pst*I genomic clone, and pBluescript which lacks a cloned insert, respectively.

10 Figure 25 depicts a Northern blot analysis of AD16c mRNA in AD and aged control brains. The data shows elevated levels of AD16c mRNA expression in 6 of 9 AD compared to 1 of 6 age-matched controls.

Figure 26 depicts a Western blot analysis of AD10-7 fusion proteins using monoclonal antibodies against the expressed tag protein (T7-tag mouse monoclonal antibodies).

15 Figure 27 (panels A and B) depicts brightfield and darkfield microscopic analysis of the *in situ* hybridization of sense and antisense cRNA probes to human brain tissue sections of early AD.

### ***Definitions***

20 In the description that follows, a number of terms used in recombinant DNA technology are utilized extensively. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided.

25 ***Cloning vector.*** A plasmid or phage DNA or other DNA sequence which is able to replicate autonomously in a host cell, and which is characterized by one or a small number of restriction endonuclease recognition sites at which such DNA sequences may be cut in a determinable fashion without loss of an essential biological function of the vector, and into which a DNA fragment may be spliced in order to bring about its replication and cloning. The cloning vector may further contain a marker suitable for use in

the identification of cells transformed with the cloning vector. Markers, for example, provide tetracycline resistance or ampicillin resistance.

**Expression vector.** A vector similar to a cloning vector but which is capable of enhancing the expression of a gene which has been cloned into it, after transformation into a host. The cloned gene is usually placed under the control of (i.e., operably linked to) certain control sequences such as promoter sequences. Promoter sequences may be either constitutive or inducible.

**Substantially pure.** As used herein means that the desired purified protein is essentially free from contaminating cellular components, said components being associated with the desired protein in nature, as evidenced by a single band following polyacrylamide-sodium dodecyl sulfate gel electrophoresis. Contaminating cellular components may include, but are not limited to, proteinaceous, carbohydrate, or lipid impurities.

The term "substantially pure" is further meant to describe a molecule which is homogeneous by one or more purity or homogeneity characteristics used by those of skill in the art. For example, a substantially pure NTP will show constant and reproducible characteristics within standard experimental deviations for parameters such as the following: molecular weight, chromatographic migration, amino acid composition, amino acid sequence, blocked or unblocked N-terminus, HPLC elution profile, biological activity, and other such parameters. The term, however, is not meant to exclude artificial or synthetic mixtures of the factor with other compounds. In addition, the term is not meant to exclude NTP fusion proteins isolated from a recombinant host.

**Recombinant Host.** According to the invention, a recombinant host may be any prokaryotic or eukaryotic cell which contains the desired cloned genes on an expression vector or cloning vector. This term is also meant to include those prokaryotic or eukaryotic cells that have been genetically engineered to contain the desired gene(s) in the chromosome or genome of that organism.



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**Recombinant vector.** Any cloning vector or expression vector which contains the desired cloned gene(s).

**Host.** Any prokaryotic or eukaryotic cell that is the recipient of a replicable expression vector or cloning vector. A "host," as the term is used herein, also includes prokaryotic or eukaryotic cells that can be genetically engineered by well known techniques to contain desired gene(s) on its chromosome or genome. For examples of such hosts, see Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1989).

**Promoter.** A DNA sequence generally described as the 5' region of a gene, located proximal to the start codon. The transcription of an adjacent gene(s) is initiated at the promoter region. If a promoter is an inducible promoter, then the rate of transcription increases in response to an inducing agent. In contrast, the rate of transcription is not regulated by an inducing agent if the promoter is a constitutive promoter.

**Gene.** A DNA sequence that contains information needed for expressing a polypeptide or protein.

**Structural gene.** A DNA sequence that is transcribed into messenger RNA (mRNA) that is then translated into a sequence of amino acids characteristic of a specific polypeptide.

**Antisense RNA gene/Antisense RNA.** In eukaryotes, mRNA is transcribed by RNA polymerase II. However, it is also known that one may construct a gene containing a RNA polymerase II template wherein a RNA sequence is transcribed which has a sequence complementary to that of a specific mRNA but is not normally translated. Such a gene construct is herein termed an "antisense RNA gene" and such a RNA transcript is termed an "antisense RNA." Antisense RNAs are not normally translatable due to the presence of translation stop codons in the antisense RNA sequence.

**Antisense oligonucleotide.** A DNA or RNA molecule containing a nucleotide sequence which is complementary to that of a specific mRNA. An

antisense oligonucleotide binds to the complementary sequence in a specific mRNA and inhibits translation of the mRNA.

**Antisense Therapy.** A method of treatment wherein antisense oligonucleotides are administered to a patient in order to inhibit the expression of the corresponding protein.

**Complementary DNA (cDNA).** A "complementary DNA," or "cDNA" gene includes recombinant genes synthesized by reverse transcription of mRNA and from which intervening sequences (introns) have been removed.

**Expression.** Expression is the process by which a polypeptide is produced from a structural gene. The process involves transcription of the gene into mRNA and the translation of such mRNA into polypeptide(s).

**Homologous/Nonhomologous** Two nucleic acid molecules are considered to be "homologous" if their nucleotide sequences share a similarity of greater than 50%, as determined by HASH-coding algorithms (Wilber, W.J. and Lipman, D.J., *Proc. Natl. Acad. Sci.* 80:726-730 (1983)). Two nucleic acid molecules are considered to be "nonhomologous" if their nucleotide sequences share a similarity of less than 50%.

**Ribozyme.** A ribozyme is an RNA molecule that contains a catalytic center. The term includes RNA enzymes, self-splicing RNAs, and self-cleaving RNAs.

**Ribozyme Therapy.** A method of treatment wherein ribozyme is administered to a patient in order to inhibit the translation of the target mRNA.

**Fragment.** A "fragment" of a molecule such as NTP is meant to refer to any polypeptide subset of that molecule.

**Functional Derivative.** The term "functional derivatives" is intended to include the "variants," "analogues," or "chemical derivatives" of the molecule. A "variant" of a molecule such as NTP is meant to refer to a naturally occurring molecule substantially similar to either the entire molecule, or a fragment thereof. An "analogue" of a molecule such as NTP is meant to

refer to a non-natural molecule substantially similar to either the entire molecule or a fragment thereof.

A molecule is said to be "substantially similar" to another molecule if the sequence of amino acids in both molecules is substantially the same, and if both molecules possess a similar biological activity. Thus, provided that two molecules possess a similar activity, they are considered variants as that term is used herein even if one of the molecules contains additional amino acid residues not found in the other, or if the sequence of amino acid residues is not identical.

As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half-life, etc. The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, etc. Examples of moieties capable of mediating such effects are disclosed in *Remington's Pharmaceutical Sciences* (1980) and will be apparent to those of ordinary skill in the art.

**NTP.** The term "NTP" refers to a family of neural thread proteins. The NTP family includes proteins with molecular weights of about 8 kDa, 14 kDa, 17 kDa, 21 kDa, 26 kDa and 42 kDa, as described herein.

**Immuno-Polymerase Chain Reaction.** A method for the detection of antigens using specific antibody-DNA conjugates. According to this method, a linker molecule with bispecific binding affinity for DNA and antibodies is used to attach a DNA molecule specifically to an antigen-antibody complex. As a result, a specific antigen-antibody-DNA conjugate is formed. The attached DNA can be amplified by the polymerase chain reaction (PCR) using appropriate oligonucleotide primers. The presence of specific PCR products demonstrates that DNA molecules are attached specifically to antigen-antibody complexes, thus indicating the presence of antigen. (Sano *et al.*, *Science* 258:120-122 (1992)).

For example, Sano *et al.*, *supra*, constructed a streptavidin-protein A chimera that possesses specific binding affinity for biotin and immunoglobulin G. This chimera (i.e., the "linker molecule") was used to attach a biotinylated DNA specifically to antigen-monoclonal antibody complexes that had been immobilized on microtiter plate wells. A segment of the attached DNA was subsequently amplified by PCR.

### *Detailed Description of the Invention*

This invention is directed to neural thread proteins (NTP), genetic sequences coding for an NTP mRNA or antisense mRNA, expression vectors containing the genetic sequences, recombinant hosts transformed therewith, and NTP and antisense RNA produced by such transformed recombinant host expression. This invention further relates to NTP ribozymes, and recombinant DNA molecules which code for NTP ribozymes and NTP antisense oligonucleotides. This invention further relates to antibodies directed against an NTP, as well as the use of NTP antibodies and NTP nucleic acid sequences for detection of the presence of an NTP in biological samples. The invention further relates to the use of NTP coding sequences in gene therapy.

#### *I. Isolation of DNA Sequences Coding for Neuronal Thread Proteins*

DNA sequences coding for an NTP are derived from a variety of sources. These sources include genomic DNA, cDNA, synthetic DNA, and combinations thereof.

Human NTP genomic DNA can be extracted and purified from any human cell or tissue, by means well known in the art (for example, *see* Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989). The NTP genomic DNA of the invention may or may not include naturally occurring introns. Moreover, such genomic DNA may be obtained in association with the 5' promoter region of

the NTP gene sequences and/or with the 3' translational termination region. Further, such genomic DNA may be obtained in association with DNA sequences which encode the 5' nontranslated region of the NTP mRNA and/or with the genetic sequences which encode the 3' nontranslated region. To the extent that a host cell can recognize the transcriptional and/or translational regulatory signals associated with the expression of the mRNA and protein, then the 5' and/or 3' nontranscribed regions of the native gene, and/or, the 5' and/or 3' nontranslated regions of the mRNA, may be retained and employed for transcriptional and translational regulation.

Alternatively, an NTP mRNA can be isolated from any cell which expresses an NTP, and used to produce cDNA by means well known in the art (for example, *see* Sambrook *et al.*, *supra*). Preferably, the mRNA preparation used will be enriched in mRNA coding for an NTP, either naturally, by isolation from cells which produce large amounts of an NTP, or *in vitro*, by techniques commonly used to enrich mRNA preparations for specific sequences, such as sucrose gradient centrifugation, or both. An NTP mRNA may be obtained from mammalian neuronal tissue, or from cell lines derived therefrom. Preferably, human cDNA libraries are constructed from 17-18 week old fetal brain, 2 year old temporal lobe neocortex, end-stage AD cerebral cortex, or from cell lines derived from human neuronal tissue. Such cell lines may include, but are not limited to, central nervous system primitive neuroectodermal tumor cells (such as PNET1 or PNET2, as described herein), neuroblastoma cells (such as SH-Sy5y, as described herein), or human glioma cells (such as A172; ATCC CRL 1620). Alternatively, a rat cDNA library can be prepared from mRNA isolated from rat glioma cells, for example, C6 rat glioma cells (ATCC CCL107).

For cloning into a vector, suitable DNA preparations (either genomic or cDNA) are randomly sheared or enzymatically cleaved, respectively, and ligated into appropriate vectors to form a recombinant gene (either genomic or cDNA) library. A DNA sequence encoding an NTP may be inserted into a vector in accordance with conventional techniques, including blunt-ending

or staggered-ending termini for ligation, restriction enzyme digestion to provide appropriate termini, filling in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and ligation with appropriate ligases. Techniques for such manipulation are disclosed by  
5 Sambrook *et al.*, *supra*, and are well known in the art.

Libraries containing NTP clones may be screened and the NTP clones identified by any means which specifically selects for NTP DNA such as, for example: 1) by hybridization with an appropriate nucleic acid probe(s) containing a sequence specific for the DNA of this protein; or, 2) by  
10 hybridization-selected translational analysis in which native mRNA hybridizes to the clone in question, is translated *in vitro*, and the translation products are further characterized; or, 3) if the cloned DNA sequences are themselves capable of expressing mRNA, by immunoprecipitation of a translated NTP product produced by the host containing the clone.

15 Oligonucleotide probes specific for an NTP which can be used to identify clones to this protein can be designed from knowledge of the amino acid sequence of the corresponding NTP, or homologous regions of the PTP. Alternatively, oligonucleotide probes can be designed from knowledge of the nucleotide sequence of PTP (de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013  
20 (1990)).

The suitable oligonucleotide, or set of oligonucleotides, which is capable of encoding a fragment of the NTP gene (or which is complementary to such an oligonucleotide, or set of oligonucleotides) may be synthesized by means well known in the art (for example, see Sambrook *et al.*, *supra*).  
25 Techniques of nucleic acid hybridization and clone identification are disclosed by Sambrook *et al.*, *supra*. Those members of the above-described gene library which are found to be capable of such hybridization are then analyzed to determine the extent and nature of the NTP encoding sequences which they contain.

30 To facilitate the detection of the desired NTP coding sequence, the above-described DNA probe is labeled with a detectable group. Such

detectable group can be any material having a detectable physical or chemical property. Such materials have been well-developed in the field of nucleic acid hybridization and in general most any label useful in such methods can be applied to the present invention. Particularly useful are radioactive labels including  $^{32}\text{P}$ ,  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{125}\text{I}$ , or the like. Any radioactive label may be employed which provides for an adequate signal and has sufficient half-life. The DNA probe may be labeled, for example, by nick-translation, by T4 DNA polymerase replacement synthesis, or by random priming, among other methods well known in the art (*see Sambrook et al. supra*).

Alternatively, DNA probes can be labeled with non-radioactive markers such as biotin, an enzyme, or fluorescent group.

In an alternative method of cloning NTP DNA sequences, NTP cDNAs are obtained by direct cloning of cDNAs from cell lines and brain tissue, using the 3'- and 5'-RACE methods, as described herein. Preferably, a human neuroectodermal tumor cell line or AD brain tissue is used as a source of mRNA.

## II. *Expressing the Gene Coding for NTP*

The above-discussed methods are, therefore, capable of identifying DNA sequences which are code for an NTP or fragments thereof. In order to further characterize such DNA sequences, and in order to produce the recombinant protein, it is desirable to express the proteins which the DNA sequences encode.

To express an NTP, transcriptional and translational signals recognizable by an appropriate host are necessary. The cloned NTP DNA sequences, obtained through the methods described above, and preferably in double-stranded form, may be "operably linked" to sequences controlling transcriptional expression in an expression vector, and introduced into a host cell, either prokaryotic or eukaryotic, to produce recombinant NTP. Depending upon which strand of the NTP coding sequence is operably linked

to the sequences controlling transcriptional expression, it is also possible to express an NTP antisense RNA.

Expression of the NTP in different hosts may result in different post-translational modifications which may alter the properties of the NTP. Preferably, the present invention encompasses the expression of an NTP in eukaryotic cells, and especially mammalian, insect, and yeast cells. Especially preferred eukaryotic hosts are mammalian cells. Mammalian cells provide post-translational modifications to recombinant NTP which include folding and/or phosphorylation. Most preferably, mammalian host cells include human CNS primitive neuroectodermal tumor cells, human neuroblastoma cells, human glioma cells, or rat glioma cells. Especially preferred primitive neuroectodermal tumor cells include PNET1 and PNET2, especially preferred human glioblastoma cells include Hg16 and Hg17, especially preferred human glioma cells include A172, and especially preferred rat glioma cells include C6 (see Example 1).

Alternatively, an NTP may be expressed by prokaryotic host cells. Preferably, a recombinant NTP is expressed by such cells as a fusion protein, as described herein. An especially preferred prokaryotic host is *E. coli*. Preferred strains of *E. coli* include Y1088, Y1089, CSH18, ER1451, and ER1647 (see, for example, *Molecular Biology LabFax*, Brown, T.A., Ed., Academic Press, New York (1991)). An alternative preferred host is *Bacillus subtilis*, including such strains as BR151, YB886, M1119, M1120, and B170 (see, for example, Hardy, "Bacillus Cloning Methods," in *DNA Cloning: A Practical Approach*, IRL Press, Washington, D.C. (1985)).

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains expression control sequences which in turn contain transcriptional regulatory information and such sequences are "operably linked" to the nucleotide sequence which encodes the protein.

Two sequences of a nucleic acid molecule are said to be operably linked when they are linked to each other in a manner which either permits both sequences to be transcribed onto the same RNA transcript, or permits an



RNA transcript, begun in one sequence to be extended into the second sequence. Thus, two sequences, such as a promoter sequence and any other "second" sequence of DNA or RNA are operably linked if transcription commencing in the promoter sequence will produce an RNA transcript of the operably linked second sequence. In order to be operably linked it is not necessary that two sequences be immediately adjacent to one another.

The promoter sequences of the present invention may be either prokaryotic, eukaryotic or viral. Suitable promoters are repressible, constitutive, or inducible. Examples of suitable prokaryotic promoters include promoters capable of recognizing the T4 polymerases (Malik *et al.*, *J. Biol. Chem.* 263:1174-1181 (1984); Rosenberg *et al.*, *Gene* 59:191-200 (1987); Shinedling *et al.*, *J. Molec. Biol.* 195:471-480 (1987); Hu *et al.*, *Gene* 42:21-30 (1986)), T3, Sp6, and T7 (Chamberlin *et al.*, *Nature* 228:227-231 (1970); Bailey *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 80:2814-2818 (1983); Davanloo *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 81:2035-2039 (1984)); the P<sub>R</sub> and P<sub>L</sub> promoters of bacteriophage lambda (*The Bacteriophage Lambda*, Hershey, A.D., Ed., Cold Spring Harbor Press, Cold Spring Harbor, NY (1973); *Lambda II*, Hendrix, R.W., Ed., Cold Spring Harbor Press, Cold Spring Harbor, NY (1980)); the trp, recA, heat shock, and lacZ promoters of *E. coli*; the  $\alpha$ -amylase (Ulmanen *et al.*, *J. Bacteriol.* 162:176-182 (1985)) and the delta-28-specific promoters of *B. subtilis* (Gilman *et al.*, *Gene* 32:11-20 (1984)); the promoters of the bacteriophages of *Bacillus* (Gryczan, In: *The Molecular Biology of the Bacilli*, Academic Press, Inc., NY (1982)); *Streptomyces* promoters (Ward *et al.*, *Mol. Gen. Genet.* 203:468-478 (1986)); the *int* promoter of bacteriophage lambda; the *bla* promoter of the  $\beta$ -lactamase gene of pBR322, and the CAT promoter of the chloramphenicol acetyl transferase gene of pBR325, etc. Prokaryotic promoters are reviewed by Glick, *J. Ind. Microbiol.* 1:277-282 (1987); Cenatiempo, *Biochimie* 68:505-516 (1986); Watson *et al.*, In: *Molecular Biology of the Gene*, Fourth Edition, Benjamin Cummins, Menlo Park, CA (1987); Gottesman, *Ann. Rev. Genet.* 18:415-442 (1984); and Sambrook *et al.*, *supra*.

Preferred eukaryotic promoters include the promoter of the mouse metallothionein I gene (Hamer *et al.*, *J. Mol. Appl. Gen.* 1:273-288 (1982)); the TK promoter of Herpes virus (McKnight, *Cell* 31:355-365 (1982)); the SV40 early promoter (Benoist, *et al.*, *Nature (London)* 290:304-310 (1981)); and the yeast *gal4* gene promoter (Johnston, *et al.*, *Proc. Natl. Acad. Sci. (USA)* 79:6971-6975 (1982); Silver, *et al.*, *Proc. Natl. Acad. Sci. (USA)* 81:5951-5955 (1984)). All of the above listed references are incorporated by reference herein.

Strong promoters are the most preferred promoters of the present invention. Examples of such preferred promoters are those which recognize the T3, SP6 and T7 polymerase promoters; the  $P_L$  promoter of bacteriophage lambda; the *recA* promoter and the promoter of the mouse metallothionein I gene. The most preferred promoter for expression in prokaryotic cells is one which is capable of recognizing the T7 polymerase promoter. The sequences of such polymerase recognition sequences are disclosed by Watson, *et al.* (In: *Molecular Biology of the Gene*, Fourth Edition, Benjamin Cummins, Menlo Park, CA, (1987)). The most preferred promoter for expression in mammalian cells is SV40 (Gorman, "High Efficiency Gene Transfer into Mammalian cells," in *DNA Cloning: A Practical Approach*, Volume II, IRL Press, Washington, D.C., pp. 143-190 (1985)).

### *III. Methods of Detecting NTP*

This invention is directed towards methods of detecting neurological disease in a human subject, utilizing the nucleic acid probes hybridizable to NTP genes or transcripts, or antibodies specific for an NTP. By "neurological disease" is meant Alzheimer's Disease (AD), or other neurodegenerative disorders with the Alzheimer's type pathogenic changes (for example, Parkinson's disease with AD-type neurodegeneration), as well as neuroectodermal tumors, malignant astrocytomas, and glioblastomas. By "human subject" is meant any human being or any developmental form thereof, such as a human embryo or fetus, prior to birth. The diagnostic methods of the present invention do not require invasive removal of neural tissue.

The present invention additionally pertains to assays, both nucleic acid hybridization assays and immunoassays, for detecting the presence of NTP in cells or in the biological fluids of a human subject using light or electron microscopic histology, imaging, radioactive or enzyme based assays, and the like.

#### *a. Nucleic Acid Hybridization Assays*

In testing a tissue sample for an NTP using a nucleic acid hybridization assay, RNA can be isolated from tissue by sectioning on a cryostat and lysing the sections with a detergent such as SDS and a chelating agent such as EDTA, optionally with overnight digestion with proteinase K (50  $\mu$ g/ml). Such tissue is obtained by autopsy and biopsy. A preferred quantity of tissue is in the range of 1-10 milligrams. Protein is removed by phenol and chloroform extractions, and nucleic acids are precipitated with ethanol. RNA is isolated by chromatography on an oligo dT column and then eluted therefrom. Further fractionation can also be carried out, according to methods well known to those of ordinary skill in the art.

A number of techniques for molecular hybridization are used for the detection of DNA or RNA sequences in tissues; each has certain advantages and disadvantages. When large amounts of tissue are available, analysis of hybridization kinetics provides the opportunity to accurately quantitate the amount of DNA or RNA present, as well as to distinguish sequences that are closely related but not identical to the probe, and determine the percent homology.

Reactions are run under conditions of hybridization ( $T_m - 25^\circ\text{C}$ ) in which the rate of reassociation of the probe is optimal (Wetmur *et al.*, *J. Mol. Biol.* 31:349-370 (1968)). The kinetics of the reaction are second-order when the sequences in the tissue are identical to those of the probe; however, the reaction exhibits complex kinetics when probe sequences have partial homology to those in the tissue (Sharp *et al.*, *J. Mol. Biol.* 86:709-726 (1974)).

The ratio of probe to cell RNA is determined by the sensitivity desired. To detect one transcript per cell would require about 100 pg of probe per  $\mu\text{g}$  of total cellular DNA or RNA. The nucleic acids are mixed, denatured, brought to the appropriate salt concentration and temperature, and allowed to hybridize for various periods of time. The rate of reassociation can be determined by quantitating the amount of probe hybridized either by hydroxyapatite chromatography (Britten *et al.*, *Science* 161:529-540 (1968)) or S1 nuclease digestion (Sutton, *Biochim. Biophys. Acta* 240:522-531 (1971)).

A more flexible method of hybridization is the northern blot technique. This technique offers variability in the stringency of the hybridization reaction, as well as determination of the state of the retroviral sequences in the specimen under analysis. Northern analysis can be performed as described herein.

A major consideration associated with hybridization analysis of DNA or RNA sequences is the degree of relatedness the probe has with the sequences present in the specimen under study. This is important with the blotting technique, since a moderate degree of sequence homology under

nonstringent conditions of hybridization can yield a strong signal even though the probe and sequences in the sample represent non-homologous genes.

5 The particular hybridization technique is not essential to the invention, any technique commonly used in the art being within the scope of the present invention. Typical probe technology is described in United States Patent 4,358,535 to Falkow *et al.*, incorporated by reference herein. For example, hybridization can be carried out in a solution containing 6 x SSC (10 x SSC: 1.5 M sodium chloride, 0.15 M sodium citrate, pH 7.0), 5 x Denhardt's (1 x Denhardt's: 0.2% bovine serum albumin, 0.2% polyvinylpyrrolidone, 0.02% Ficol1 400), 10 mM EDTA, 0.5% SDS and about 10<sup>7</sup> cpm of nick-translated DNA for 16 hours at 65°C.

15 The labeled probes, as described above, provide a general diagnostic method for detection of an NTP in tissue. The method is reasonably rapid, has a simple protocol, has reagents which can be standardized and provided as commercial kits, and allows for rapid screening of large numbers of samples.

In one method for carrying out the procedure, a clinical isolate containing RNA transcripts is fixed to a support. The affixed nucleic acid is contacted with a labeled polynucleotide having a base sequence complementary or homologous to the coding strand of the NTP gene.

20 The hybridization assays of the present invention are particularly well suited for preparation and commercialization in kit form, the kit comprising a carrier means compartmentalized to receive one or more container means (vial, test tube, etc.) in close confinement, each of said container means comprising one of the separate elements to be used in hybridization assay.

25 For example, there may be a container means containing NTP cDNA molecules suitable for labeling by "nick translation" (*see, for example, Sambrook et al., supra*, for standard methodology), or labeled NTP cDNA or RNA molecules. Further container means may contain standard solutions for nick translation of NTP cDNA comprising DNA polymerase I/DNase I and 30 unlabeled deoxyribonucleotides (i.e., dCTP, dTTP, dGTP, and dATP).

The presence of NTP RNA is determined by the variation in the appearance and/or quantity of probe-related RNA in tested tissue.

The DNA probes of this invention can also be used for differential diagnosis of hereditary or familial AD and non-hereditary or sporadic AD. The familial form of AD often occurs at an earlier age and is associated with Down's syndrome in the family. Thus, a genetic test for familial AD allows for genetic counseling of families. While much effort has been directed toward characterizing a genetic marker for familial AD (Gusella, *FASEB J* 3:2036-2041 (1989); Hooper, *J NIH Res.* 4:48-54 (1992)), genetic linkage analysis only identifies a genetic marker sequence without providing the knowledge of the function of the genomic sequence. In contrast, the cDNA probes described herein and obtained from individuals with sporadic AD encode a known protein of known function which is over-expressed in brain tissue of patients with AD.

Most cases of the AD disorder appear to be the sporadic form, although there are well-documented familial cases (Gusella, *supra*; *Harrison's Principles of Internal Medicine*, Braunwald *et al.*, Eds., Eleventh Edition, McGraw-Hill Book Company, New York, pp. 2012-2013 (1987)). A patient with familial AD, unlike a patient with sporadic AD, inherited the predisposing mutation through the germ cells. Some of the familial cases have been shown to follow an autosomal dominant pattern of inheritance (*Id.*). Thus, the DNA of a patient with familial AD will contain the inherited genetic alteration which is absent from the DNA of a patient with sporadic AD.

A method of differentiating between sporadic and familial AD in a human subject involves obtaining a biological sample from the human subject who is suspected of having Alzheimer's Disease. Then, DNA is purified from the biological sample. Finally, the DNA is contacted with a NTP DNA probe under conditions of hybridization. Familial AD is indicated by the detection of a hybrid of the probe and the DNA, whereas sporadic AD is indicated by the absence of detection of hybridization.

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For example, the biological sample can be a blood sample which is subjected to differential centrifugation to enrich for white blood cells within three days of collection (Park, "PCR in the Diagnosis of Retinoblastoma," in *PCR Protocols*, Innis *et al.*, Eds., Academic Press, Inc., New York, pp. 407-415 (1990)). The DNA sample can be prepared using the sodium N-lauroylsarcosine-Proteinase K, phenol, and RNase method (Sambrook *et al.*, *supra*). DNA analysis can be performed by digesting the DNA sample, preferably 5 micrograms, with a restriction endonuclease (such as *HindIII*). Digested DNA is then fractionated using agarose gel electrophoresis, preferably, a 1% horizontal agarose gel, for 18 hours in a buffer preferably containing 89 mM Tris-Hcl (pH 8), 89 mM sodium borate and 2 mM EDTA (Gusella *et al.*, *Nature* 306:234-238 (1983)). Southern analysis can be performed using conventional techniques (Sambrook *et al.*, *supra*), and the labelled AD cDNA probes can be hybridized under conditions described above. The preferred DNA probes for this differential diagnosis method include 1-9a, AD3-4, AD4-4 and G2-2 PstI.

*b. Immunoassays*

Antibodies directed against an NTP can be used, as taught by the present invention, to detect and diagnose AD. Various histological staining methods, including immunohistochemical staining methods, may also be used effectively according to the teaching of the invention. Silver stain is but one method of visualizing NTP. Other staining methods useful in the present invention will be obvious to the artisan, the determination of which would not involve undue experimentation (*see generally*, for example, *A Textbook of Histology*, Eds. Bloom and Fawcett, W.B. Saunders Co., Philadelphia (1964)).

One screening method for determining whether a given compound is an NTP functional derivative comprises, for example, immunoassays employing radioimmunoassay (RIA) or enzyme-linked immunosorbant assay (ELISA) methodologies, based on the production of specific antibodies

(monoclonal or polyclonal) to an NTP. For these assays, biological samples are obtained by venepuncture (blood), spinal tap (cerebral spinal fluid (CSF)), urine and other body secretions such as sweat and tears. For example, in one form of RIA, the substance under test is mixed with diluted antiserum in the presence of radiolabeled antigen. In this method, the concentration of the test substance will be inversely proportional to the amount of labeled antigen bound to the specific antibody and directly related to the amount of free labeled antigen. Other suitable screening methods will be readily apparent to those of skill in the art.

The present invention also relates to methods of detecting an NTP or functional derivatives in a sample or subject. For example, antibodies specific for an NTP, or a functional derivative, may be detectably labeled with any appropriate marker, for example, a radioisotope, an enzyme, a fluorescent label, a paramagnetic label, or a free radical.

Alternatively, antibodies specific for an NTP, or a functional derivative, may be detectably labeled with DNA by the technique of immunopolymerase chain reaction (Sano *et al.*, *Science* 258: 120-122 (1992)). The polymerase chain reaction (PCR) procedure amplifies specific nucleic acid sequences through a series of manipulations including denaturation, annealing of oligonucleotide primers, and extension of the primers with DNA polymerase (*see*, for example, Mullis *et al.*, U.S. Patent No. 4,683,202; Mullis *et al.*, U.S. Patent No. 4,683,195; Loh *et al.*, *Science* 243:217 (1988)). The steps can be repeated many times, resulting in a large amplification of the number of copies of the original specific sequence. As little as a single copy of a DNA sequence can be amplified to produce hundreds of nanograms of product (Li *et al.*, *Nature* 335:414 (1988)). Other known nucleic acid amplification procedures include transcription-based amplification systems (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989); Gingeras *et al.*, WO 88/10315), and the "ligase chain reaction" in which two (or more) oligonucleotides are ligated in the presence of a nucleic acid target having the sequence of the resulting "di-oligonucleotide" thereby amplifying the di-



oligonucleotide (Wu *et al.*, *Genomics* 4:560 (1989); Backman *et al.*, EP 320,308; Wallace, EP 336,731; Orgel, WO 89/09835). For example, the immuno-PCR assay can be carried out by immobilizing various amounts of the test material on the surface of microtiter wells (*see* Sanzo *et al.*, *supra*, page 122, footnote 7). The wells are subsequently incubated with an NTP monoclonal antibody, washed, and then incubated with biotinylated NTP DNA molecules which have been conjugated to streptavidin-protein chimera (*Id.*). This chimera binds biotin (via the streptavidin moiety) and the Fc portion of an immunoglobulin G molecule (via the protein A moiety) (*Id.*, at 120; Sanzo *et al.*, *Bio/Technology* 9:1378 (1991)). The wells are then washed to remove unbound conjugates. Any NTP present in the test material will be bound by the NTP monoclonal antibody, which in turn, is bound by the protein A moiety of the biotinylated NTP DNA - streptavidin-protein A conjugate. Then, the NTP DNA sequences are amplified using PCR. Briefly, the microtiter wells are incubated with deoxyribonucleoside triphosphates, NTP oligonucleotide primers, and Taq DNA polymerase (*see* Sanzo *et al.*, *supra*, page 122, footnote 11). An automated thermal cycler (such as the PTC-100-96 Thermal Cycler, MJ Research, Inc.) can be used to perform PCR under standard conditions (*Id.*). The PCR products are then analyzed by agarose gel electrophoresis after staining with ethidium bromide.

Methods of making and detecting such detectably labeled antibodies or their functional derivatives are well known to those of ordinary skill in the art, and are described in more detail below. Standard reference works setting forth the general principles of immunology include the work of Klein (*Immunology: The Science of Self-Nonself Discrimination*, John Wiley & Sons, New York (1982)); Kennett *et al.* (*Monoclonal Antibodies and Hybridomas: A New Dimension in Biological Analyses*, Plenum Press, New York (1980)); Campbell ("Monoclonal Antibody Technology," In: *Laboratory Techniques in Biochemistry and Molecular Biology*, Volume 13 (Burdon, R., *et al.*, eds.), Elsevier, Amsterdam (1984)); and Eisen (In: *Microbiology*, 3rd Ed. (Davis, *et al.*, Harper & Row, Philadelphia (1980)).

The term "antibody" refers both to monoclonal antibodies which are a substantially homogeneous population and to polyclonal antibodies which are heterogeneous populations. Polyclonal antibodies are derived from the sera of animals immunized with an antigen. Monoclonal antibodies (mAbs) to specific antigens may be obtained by methods known to those skilled in the art. See, for example, Kohler and Milstein, *Nature* 256:495-497 (1975) and U.S. Patent No. 4,376,110. Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof.

The monoclonal antibodies, particularly mAbs Th7, Th9, and Th10 used in the present invention, may be prepared as previously described (Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985); Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). The Th monoclonal antibodies were generated against the purified pancreatic form of thread protein (*Id.*). NTP-specific polyclonal and monoclonal antibodies can also be generated against a substantially pure NTP isolated from recombinant hosts (for example, see Carroll *et al.*, "Production and Purification of Polyclonal Antibodies to the Foreign Segment of  $\beta$ -Galactosidase Fusion Proteins," in *DNA Cloning: A Practical Approach*, Volume III, IRL Press, Washington, D.C., pp. 89-111 (1987); Mole *et al.*, "Production of Monoclonal Antibodies Against Fusion Proteins Produced in *Escherichia coli*," in *DNA Cloning: A Practical Approach*, Volume III, IRL Press, Washington, D.C., pp. 113-1139 (1987)). Alternatively, NTP-specific polyclonal and monoclonal antibodies can be generated against a substantially pure NTP isolated from biological material such as brain tissue and cell lines, by using well known techniques.

For example, monoclonal antibodies specific for the various NTP molecules of approximately, 8, 14, 17, 21, 26 kDa and 42 kDa molecular weights may be prepared from recombinant-derived proteins, which are expressed, isolated and purified from the cDNA (i.e., 1-9a), genomic clones (G2-2 *Pst*I) and AD-NTP 3-4 cDNA clones. These NTP molecules are

derived from the above cDNA's and genomic clones, inserted and produced in suitable expression vectors (see Figures 2A and 2B). Since there are regions of 60-70% homology in the 5' ends of the 1-9a NTP cDNA and PTP, one can obtain monoclonal antibodies that bind specifically to the NTP recombinant proteins and not to the pancreatic form by performing routine differential screening (see, for example, de la Monte *et al.*, *J. Clin. Invest.* 86: 1004-1013 (1990)). Although there will be monoclonal antibodies that bind to both NTP and PTP, it will be possible to generate NTP-specific monoclonal antibodies because there is a substantial sequence divergence between NTP molecules of various forms (e.g., 8, 14, 17, 21, 26 and 42 kDa) and because an epitope may be defined by as few as 6-8 amino acids.

The term "antibody" is also meant to include both intact molecules as well as fragments thereof, such as, for example, Fab and F(ab')<sub>2</sub>, which are capable of binding antigen. Fab and F(ab')<sub>2</sub> fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody (Wahl *et al.*, *J. Nucl. Med.* 24:316-325 (1983)).

It will be appreciated that Fab and F(ab')<sub>2</sub> and other fragments of the antibodies useful in the present invention may be used for the detection and quantitation of an NTP according to the methods disclosed herein in order to detect and diagnose AD in the same manner as an intact antibody. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')<sub>2</sub> fragments).

An antibody is said to be "capable of binding" a molecule if it is capable of specifically reacting with the molecule to thereby bind the molecule to the antibody. The term "epitope" is meant to refer to that portion of any molecule capable of being bound by an antibody which can also be recognized by that antibody. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and have specific three dimensional structural characteristics as well as specific charge characteristics.

An "antigen" is a molecule capable of being bound by an antibody which is additionally capable of inducing an animal to produce antibody capable of binding to an epitope of that antigen. An antigen may have one, or more than one epitope. The specific reaction referred to above is meant to indicate that the antigen will react, in a highly selective manner, with its corresponding antibody and not with the multitude of other antibodies which may be evoked by other antigens.

The antibodies, or fragments of antibodies, useful in the present invention may be used to quantitatively or qualitatively detect the presence of cells which contain the NTP antigens. Thus, the antibodies (or fragments thereof) useful in the present invention may be employed histologically to detect or visualize the presence of an NTP.

Such an assay for an NTP typically comprises incubating a biological sample from said subject suspected of having such a condition in the presence of a detectably labeled binding molecule (e.g., antibody) capable of identifying an NTP, and detecting said binding molecule which is bound in a sample.

Thus, in this aspect of the invention, a biological sample may be treated with nitrocellulose, or other solid support which is capable of immobilizing cells, cell particles or soluble proteins. The support may then be washed with suitable buffers followed by treatment with the detectably labeled NTP-specific antibody. The solid phase support may then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on said solid support may then be detected by conventional means.

By "solid phase support" is intended any support capable of binding antigen or antibodies. Well-known supports, or carriers, include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical,

as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will note many other suitable carriers for binding monoclonal antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One embodiment for carrying out the diagnostic assay of the present invention on a biological sample containing an NTP, comprises:

(a) contacting a detectably labeled NTP-specific antibody with a solid support to effect immobilization of said NTP-specific antibody or a fragment thereof;

(b) contacting a sample suspected of containing an NTP with said solid support;

(c) incubating said detectably labeled NTP-specific antibody with said support for a time sufficient to allow the immobilized NTP-specific antibody to bind to the NTP;

(d) separating the solid phase support from the incubation mixture obtained in step (c); and

(e) detecting the bound label and thereby detecting and quantifying NTP.

Alternatively, labeled NTP-specific antibody/NTP complexes in a sample may be separated from a reaction mixture by contacting the complex with an immobilized antibody or protein which is specific for an immunoglobulin, e.g., *Staphylococcus* protein A, *Staphylococcus* protein G, anti-IgM or anti-IgG antibodies. Such anti-immunoglobulin antibodies may be polyclonal, but are preferably monoclonal. The solid support may then be washed with a suitable buffer to give an immobilized NTP/labeled NTP-specific antibody complex. The label may then be detected to give a measure of an NTP.

This aspect of the invention relates to a method for detecting an NTP or a fragment thereof in a sample comprising:

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- (a) contacting a sample suspected of containing an NTP with an NTP-specific antibody or fragment thereof which binds to NTP; and
- (b) detecting whether a complex is formed.

5       The invention also relates to a method of detecting an NTP in a sample, further comprising:

- (c) contacting the mixture obtained in step (a) with an Fc binding molecule, such as an antibody, *Staphylococcus* protein A, or *Staphylococcus* protein G, which is  
10       immobilized on a solid phase support and is specific for the NTP-specific antibody to give a NTP/NTP-specific antibody immobilized antibody complex;
- (d) washing the solid phase support obtained in step (c) to remove unbound NTP/NTP-specific antibody complex;
- 15       (e) and detecting the label bound to said solid support.

Of course, the specific concentrations of detectably labeled antibody and NTP, the temperature and time of incubation, as well as other assay conditions may be varied, depending on various factors including the concentration of an NTP in the sample, the nature of the sample, and the like.  
20       The binding activity of a given lot of anti-NTP antibody may be determined according to well known methods. Those skilled in the art will be able to determine operative and optimal assay conditions for each determination by employing routine experimentation.

Other such steps as washing, stirring, shaking, filtering and the like  
25       may be added to the assays as is customary or necessary for the particular situation.

One of the ways in which the NTP-specific antibody can be detectably labeled is by linking the same to an enzyme. This enzyme, in turn, when later exposed to its substrate, will react with the substrate in such a manner as to  
30       produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorometric or by visual means. Enzymes which can be

used to detectably label the NTP-specific antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-V-steroid isomerase, yeast alcohol dehydrogenase,  $\alpha$ -glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase,  $\beta$ -galactosidase, ribonuclease, urease, catalase, glucose-VI-phosphate dehydrogenase, glucoamylase and acetylcholinesterase.

Detection may be accomplished using any of a variety of immunoassays. For example, by radioactively labeling the NTP-specific antibodies or antibody fragments, it is possible to detect NTP through the use of radioimmune assays. A good description of a radioimmune assay may be found in *Laboratory Techniques and Biochemistry in Molecular Biology*, by Work, *et al.*, North Holland Publishing Company, NY (1978), with particular reference to the chapter entitled "An Introduction to Radioimmune Assay and Related Techniques" by Chard, incorporated by reference herein.

The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography. Isotopes which are particularly useful for the purpose of the present invention are:  $^3\text{H}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , and preferably  $^{125}\text{I}$ .

It is also possible to label the NTP-specific antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labelling compounds are fluorescein isothiocyanate, rhodamine, phycoerytherin, phycocyanin, allophycocyanin, *o*-phthaldehyde and fluorescamine.

The NTP-specific antibody can also be detectably labeled using fluorescence emitting metals such as  $^{152}\text{Eu}$ , or others of the lanthanide series. These metals can be attached to the NTP-specific antibody using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

The NTP-specific antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-

tagged NTP-specific antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

The NTP-specific antibody may also be labeled with biotin and then reacted with avidin. A biotin-labeled DNA fragment will be linked to the NTP-biotinylated monoclonal antibody by an avidin bridge. NTP molecules are then detected by polymerase chain reaction (PCR) amplification of the DNA fragment with specific primers (Sano *et al.*, *Science* 258: 120-122 (1992)).

Likewise, a bioluminescent compound may be used to label the NTP-specific antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Detection of the NTP-specific antibody may be accomplished by a scintillation counter, for example, if the detectable label is a radioactive gamma emitter, or by a fluorometer, for example, if the label is a fluorescent material. In the case of an enzyme label, the detection can be accomplished by colorimetric methods which employ a substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

The detection of foci of such detectably labeled antibodies is indicative of a disease or dysfunctional state as previously described. For the purposes of the present invention, the NTP which is detected by this assay may be present in a biological sample. Any sample containing an NTP can be used. However, one of the benefits of the present diagnostic invention is that invasive tissue removal may be avoided. Therefore, preferably, the sample



is a biological solution such as, for example, cerebrospinal fluid, amniotic fluid, blood, serum, urine and the like. However, the invention is not limited to assays using only these samples, it being possible for one of ordinary skill in the art to determine suitable conditions which allow the use of other samples.

For example, the three-site monoclonal antibody-based immunoradiometric assays (M-IRMA) may be used to measure NTP levels in a biological fluid, such as CSF. It is possible to obtain, by spinal tap, on a routine basis, CSF from individuals suspected of having AD. Thus, the diagnosis of AD can be established by a simple, non-invasive immunoassay which reveals NTP levels greatly increased over normal levels.

In one embodiment, as described above, this examination for AD is accomplished by removing samples of biological fluid and incubating such samples in the presence of detectably labeled antibodies (or antibody fragments). In a preferred embodiment, this technique is accomplished in a non-invasive manner through the use of magnetic imaging, fluorography, etc.

Preferably, the detection of cells which express an NTP may be accomplished by *in vivo* imaging techniques, in which the labeled antibodies (or fragments thereof) are provided to a subject, and the presence of the NTP is detected without the prior removal of any tissue sample. Such *in vivo* detection procedures have the advantage of being less invasive than other detection methods, and are, moreover, capable of detecting the presence of NTP in tissue which cannot be easily removed from the patient, such as brain tissue.

Using *in vivo* imaging techniques, it will be possible to differentiate between AD and a brain tumor because NTP will be detected throughout the brain in an AD patient, while NTP will be localized in discrete deposits in the case of brain tumors. For example, in brains of AD patients, NTP will be found in the temporal, parietal and frontal cortices as well as the amygdala and hippocampus. Favored sites for astrocytomas include the cerebrum, cerebellum, thalamus, optic chiasma, and pons (*Harrison's Principles of*

*Internal Medicine*, Petersdorf *et al.*, Eds., Tenth Edition, McGraw-Hill Book Company, New York, p.2076 (1983)), and glioblastoma multiforme is predominantly cerebral in location (*Id.* at 2075).

5 There are many different *in vivo* labels and methods of labeling known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present invention include radioactive isotopes and paramagnetic isotopes. Those of ordinary skill in the art will know of other suitable labels for binding to the antibodies used in the invention, or will be able to ascertain such, using routine experimentation. Furthermore, the binding of these labels  
10 to the antibodies can be done using standard techniques common to those of ordinary skill in the art.

An important factor in selecting a radionuclide for *in vivo* diagnosis is that the half-life of a radionuclide be long enough so that it is still detectable at the time of maximum uptake by the target, but short enough so that  
15 deleterious radiation upon the host is minimized. Ideally, a radionuclide used for *in vivo* imaging will lack a particulate emission, but produce a large number of photons in the 140-200 keV range, which maybe readily detected by conventional gamma cameras.

For *in vivo* diagnosis radionuclides may be bound to antibody either  
20 directly or indirectly by using an intermediary functional group. Intermediary functional groups which are often used in binding radioisotopes which exist as metallic ions to immunoglobulins are DTPA and EDTA. Typical examples of ions which can be bound to immunoglobulins are  $^{99m}\text{Tc}$ ,  $^{123}\text{I}$ ,  $^{111}\text{In}$ ,  $^{131}\text{I}$ ,  $^{97}\text{Ru}$ ,  $^{67}\text{Cu}$ ,  $^{67}\text{Ga}$ ,  $^{125}\text{I}$ ,  $^{68}\text{Ga}$ ,  $^{72}\text{As}$ ,  $^{89}\text{Zr}$ , and  $^{201}\text{Tl}$ .

25 For diagnostic *in vivo* imaging, the type of detection instrument available is a major factor in selecting a given radionuclide. The radionuclide chosen must have a type of decay which is detectable for a given type of instrument. In general, any conventional method for visualizing diagnostic imaging can be utilized in accordance with this invention. For example, PET,  
30 gamma, beta, and MRI detectors can be used to visualize diagnostic imaging.

The antibodies useful in the invention can also be labeled with paramagnetic isotopes for purposes of *in vivo* diagnosis. Elements which are particularly useful, as in Magnetic Resonance Imaging (MRI), include  $^{157}\text{Gd}$ ,  $^{55}\text{Mn}$ ,  $^{162}\text{Dy}$ , and  $^{56}\text{Fe}$ .

5        The antibodies (or fragments thereof) useful in the present invention are also particularly suited for use in *in vitro* immunoassays to detect the presence of an NTP in body tissue, fluids (such as CSF), or cellular extracts. In such immunoassays, the antibodies (or antibody fragments) may be utilized in liquid phase or, preferably, bound to a solid-phase carrier, as described above.

10        Those of ordinary skill in the art will know of other suitable labels which may be employed in accordance with the present invention. The binding of these labels to antibodies or fragments thereof can be accomplished using standard techniques commonly known to those of ordinary skill in the art. Typical techniques are described by Kennedy, *et al.* (*Clin. Chim. Acta* 15 70:1-31 (1976)) and Schurs, *et al.* (*Clin. Chim. Acta* 81:1-40 (1977)). Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

20        *In situ* detection may be accomplished by removing a histological specimen from a patient, and providing the combination of labeled antibodies of the present invention to such a specimen. The antibody (or fragment) is preferably provided by applying or by overlaying the labeled antibody (or fragment) to a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of an NTP, but also the 25 distribution of an NTP on the examined tissue. Using the present invention, those of ordinary skill will readily perceive that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve such *in situ* detection.

30        The binding molecules of the present invention may be adapted for utilization in an immunometric assay, also known as a "two-site" or

"sandwich" assay. In a typical immunometric assay, a quantity of unlabeled antibody (or fragment of antibody) is bound to a solid support that is insoluble in the fluid being tested (i.e., CSF) and a quantity of detectably labeled soluble antibody is added to permit detection and/or quantitation of the ternary complex formed between solid-phase antibody, antigen, and labeled antibody.

Typical, and preferred, immunometric assays include "forward" assays in which the antibody bound to the solid phase is first contacted with the sample being tested to extract the antigen from the sample by formation of a binary solid phase antibody-antigen complex. After a suitable incubation period, the solid support is washed to remove the residue of the fluid sample, including unreacted antigen, if any, and then contacted with the solution containing an unknown quantity of labeled antibody (which functions as a "reporter molecule"). After a second incubation period to permit the labeled antibody to complex with the antigen bound to the solid support through the unlabeled antibody, the solid support is washed a second time to remove the unreacted labeled antibody. This type of forward sandwich assay may be a simple "yes/no" assay to determine whether antigen is present or may be made quantitative by comparing the measure of labeled antibody with that obtained for a standard sample containing known quantities of antigen. Such "two-site" or "sandwich" assays are described by Wide at pages 199-206 of *Radioimmune Assay Method*, edited by Kirkham and Hunter, E. & S. Livingstone, Edinburgh, 1970.

In another type of "sandwich" assay, which may also be useful with the antigens of the present invention, the so-called "simultaneous" and "reverse" assays are used. A simultaneous assay involves a single incubation step as the antibody bound to the solid support and labeled antibody are both added to the sample being tested at the same time. After the incubation is completed, the solid support is washed to remove the residue of fluid sample and uncomplexed labeled antibody. The presence of labeled antibody associated with the solid support is then determined as it would be in a conventional "forward" sandwich assay.

In the "reverse" assay, stepwise addition first of a solution of labeled antibody to the fluid sample followed by the addition of unlabeled antibody bound to a solid support after a suitable incubation period is utilized. After a second incubation, the solid phase is washed in conventional fashion to free it of the residue of the sample being tested and the solution of unreacted labeled antibody. The determination of labeled antibody associated with a solid support is then determined as in the "simultaneous" and "forward" assays.

The above-described *in vitro* or *in vivo* detection methods may be used in the detection and diagnosis of AD without the necessity of removing tissue. Such detection methods may be used to assist in the determination of the stage of neurological deterioration in AD by evaluating and comparing the concentration of an NTP in the biological sample.

As used herein, an effective amount of a diagnostic reagent (such as an antibody or antibody fragment) is one capable of achieving the desired diagnostic discrimination and will vary depending on such factors as age, condition, sex, the extent of disease of the subject, counterindications, if any, and other variables to be adjusted by the physician. The amount of such materials which are typically used in a diagnostic test are generally between 0.1 to 5 mg, and preferably between 0.1 to 0.5 mg.

The assay of the present invention is also ideally suited for the preparation of a kit. Such a kit may comprise a carrier means being compartmentalized to receive in close confinement therewith one or more container means such as vials, tubes and the like, each of said container means comprising the separate elements of the immunoassay.

For example, there may be a container means containing a first antibody immobilized on a solid phase support, and a further container means containing a second detectably labeled antibody in solution. Further container means may contain standard solutions comprising serial dilutions of the NTP to be detected. The standard solutions of an NTP may be used to prepare a standard curve with the concentration of NTP plotted on the abscissa and the

detection signal on the ordinate. The results obtained from a sample containing an NTP may be interpolated from such a plot to give the concentration of the NTP.

#### IV. *Isolation of NTP*

5           The NTP proteins or fragments of this invention may be obtained by expression from recombinant DNA as described above. Alternatively, an NTP may be purified from biological material.

          For purposes of the present invention, one method of purification which is illustrative, without being limiting, consists of the following steps.

10           A first step in the purification of an NTP includes extraction of the NTP fraction from a biological sample, such as brain tissue or CSF, in buffers, with or without solubilizing agents such as urea, formic acid, detergent, or thiocyanate.

15           A second step includes subjecting the solubilized material to ion-exchange chromatography on Mono-Q or Mono-S columns (Pharmacia LKB Biotechnology, Inc; Piscataway, NJ). Similarly, the solubilized material may be separated by any other process wherein molecules can be separated according to charge density, charge distribution and molecular size, for example. Elution of the NTP from the ion-exchange resin are monitored by  
20           an immunoassay, such as M-IRMA, on each fraction. Immunoreactive peaks would be then dialyzed, lyophilized, and subjected to molecular sieve, or gel chromatography.

25           Molecular sieve or gel chromatography is a type of partition chromatography in which separation is based on molecular size. Dextran, polyacrylamide, and agarose gels are commonly used for this type of separation. One useful gel for the present invention is Sepharose 12 (Pharmacia LKB Biotechnology, Inc.). However, other methods, known to those of skill in the art may be used to effectively separate molecules based on size.

A fourth step in a purification protocol for an NTP includes analyzing the immunoreactive peaks by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), a further gel chromatographic purification step, and staining, such as, for example, silver staining.

5 A fifth step in a purification method includes subjecting the NTP obtained after SDS-PAGE to affinity chromatography, or any other procedure based upon affinity between a substance to be isolated and a molecule to which it can specifically bind. For further purification of an NTP, affinity chromatography on Sepharose conjugated to anti-NTP mAbs (such as Th9, or  
10 specific mAbs generated against substantially pure NTP) can be used. Alternative methods, such as reverse-phase HPLC, or any other method characterized by rapid separation with good peak resolution are useful.

Another method to purify an NTP is to use concentrated CSF obtained from patients with AD. For this procedure, 30-40 milliliters are concentrated  
15 by lyophilization or Amicon filtration or the like, and subjected to two dimensional gel electrophoresis. Proteins are separated in one direction by charge in a pH gradient and then, subjected to molecular sieve chromatography in the other direction by polyacrylamide gel electrophoresis. NTP-immunoreactive proteins are identified as spots by the Th monoclonal  
20 antibodies (for example, Th 9) using Western blot analysis. The gel is cut and NTP proteins are eluted from the gel. NTP purified in this manner can be sequenced or used to make new monoclonal antibodies.

It will be appreciated that other purification steps may be substituted for the preferred method described above. Those of skill in the art will be  
25 able to devise alternate purification schemes without undue experimentation.

#### V. *Gene Therapy Using Antisense Oligonucleotides and Ribozymes*

Antisense oligonucleotides have been described as naturally occurring biological inhibitors of gene expression in both prokaryotes (Mizuno *et al.*, *Proc. Natl. Acad. Sci. USA* 81:1966-1970 (1984)) and eukaryotes (Heywood,

*Nucleic Acids Res.* 14:6771-6772 (1986)), and these sequences presumably function by hybridizing to complementary mRNA sequences, resulting in hybridization arrest of translation (Paterson, *et al.*, *Proc. Natl. Acad. Sci. USA*, 74:4370-4374 (1987)).

5           Antisense oligonucleotides are short synthetic DNA or RNA nucleotide molecules formulated to be complementary to a specific gene or RNA message. Through the binding of these oligomers to a target DNA or mRNA sequence, transcription or translation of the gene can be selectively blocked and the disease process generated by that gene can be halted (*see*, for  
10           example, Jack Cohen, *Oligodeoxynucleotides, Antisense Inhibitors of Gene Expression*, CRC Press (1989)). The cytoplasmic location of mRNA provides a target considered to be readily accessible to antisense oligodeoxynucleotides entering the cell; hence much of the work in the field has focused on RNA as a target. Currently, the use of antisense oligodeoxynucleotides provides a  
15           useful tool for exploring regulation of gene expression *in vitro* and in tissue culture (Rothenberg, *et al.*, *J. Natl. Cancer Inst.* 81:1539-1544 (1989)).

          Antisense therapy is the administration of exogenous oligonucleotides which bind to a target polynucleotide located within the cells. For example, antisense oligonucleotides may be administered systemically for anticancer  
20           therapy (Smith, International Application Publication No. WO 90/09180). As described herein, NTP-related proteins are produced by neuroectodermal tumor cells, malignant astrocytoma cells, glioblastoma cells, and in relatively high concentrations (i.e., relative to controls) in brain tissue of AD patients. Thus, NTP antisense oligonucleotides of the present invention may be active  
25           in treatment against AD, as well as neuroectodermal tumors, malignant astrocytomas, and glioblastomas.

          The NTP antisense oligonucleotides of the present invention include derivatives such as S-oligonucleotides (phosphorothioate derivatives or S-oligos, *see*, Jack Cohen, *supra*). S-oligos (nucleoside phosphorothioates) are  
30           isoelectronic analogs of an oligonucleotide (O-oligo) in which a nonbridging oxygen atom of the phosphate group is replaced by a sulfur atom. The S-



oligos of the present invention may be prepared by treatment of the corresponding O-oligos with 3H-1,2-benzodithiol-3-one-1,1-dioxide which is a sulfur transfer reagent. See Iyer *et al.*, *J. Org. Chem.* 55:4693-4698 (1990); and Iyer *et al.*, *J. Am. Chem. Soc.* 112:1253-1254 (1990), the disclosures of which are fully incorporated by reference herein.

As described herein, sequence analysis of an NTP cDNA clone shows that NTP contains sequences which are nonhomologous to PTP DNA sequences (see Figure 9). Thus, the NTP antisense oligonucleotides of the present invention may be RNA or DNA which is complementary to and stably hybridizes with such sequences which are specific for an NTP. Use of an oligonucleotide complementary to this region allows for the selective hybridization to NTP mRNA and not to mRNA specifying PTP. Preferably, the NTP antisense oligonucleotides of the present invention are a 15 to 30-mer fragment of the antisense DNA molecule coding for the nonhomologous sequences of the AD 3-4 cDNA, such as:

1. 5'-CCGATTCCAACAGACCATCAT-3' [SEQ ID NO: 1];
2. 5'-CCAACAGACCATCATTCCACC-3' [SEQ ID NO: 2]; and
3. 5'-CCAAACCGATTCCAACAGACC-3' [SEQ ID NO: 3].

Preferred antisense oligonucleotides bind to the 5'-end of the AD10-7 mRNA. Such antisense oligonucleotides may be used to down regulate or inhibit expression of the NTP gene. Examples of such antisense oligonucleotides (30-mers) include:

1. 5'-CCTGGGCAACAAGAGCGAAACTCCATCTC-3' [SEQ ID NO: 4];
2. 5'-ATCGCTTGAACCCGGGAGGCGGAGGTTGCG-3' [SEQ ID NO: 5]; and
3. 5'-GGGGAGGCTGAGGCAGGAGAATCGCTTGAA-3' [SEQ ID NO: 6].

Included as well in the present invention are pharmaceutical compositions comprising an effective amount of at least one of the NTP antisense oligonucleotides of the invention in combination with a pharma-

ceutically acceptable carrier. In one embodiment, a single NTP antisense oligonucleotide is utilized. In another embodiment, two NTP antisense oligonucleotides are utilized which are complementary to adjacent regions of the NTP genome. Administration of two NTP antisense oligonucleotides which are complementary to adjacent regions of the genome or corresponding mRNA may allow for more efficient inhibition of NTP genomic transcription or mRNA translation, resulting in more effective inhibition of NTP production.

Preferably, the NTP antisense oligonucleotide is coadministered with an agent which enhances the uptake of the antisense molecule by the cells. For example, the NTP antisense oligonucleotide may be combined with a lipophilic cationic compound which may be in the form of liposomes. The use of liposomes to introduce nucleotides into cells is taught, for example, in U.S. Patent Nos. 4,897,355 and 4,394,448, the disclosures of which are incorporated by reference in their entirety. *See also* U.S. Patent Nos. 4,235,871, 4,231,877, 4,224,179, 4,753,788, 4,673,567, 4,247,411, 4,814,270 for general methods of preparing liposomes comprising biological materials.

Alternatively, the NTP antisense oligonucleotide may be combined with a lipophilic carrier such as any one of a number of sterols including cholesterol, cholate and deoxycholic acid. A preferred sterol is cholesterol.

In addition, the NTP antisense oligonucleotide may be conjugated to a peptide that is ingested by cells. Examples of useful peptides include peptide hormones, antigens or antibodies, and peptide toxins. By choosing a peptide that is selectively taken up by the neoplastic cells, specific delivery of the antisense agent may be effected. The NTP antisense oligonucleotide may be covalently bound via the 5'OH group by formation of an activated aminoalkyl derivative. The peptide of choice may then be covalently attached to the activated NTP antisense oligonucleotide via an amino and sulfhydryl reactive hetero bifunctional reagent. The latter is bound to a cysteine residue present in the peptide. Upon exposure of cells to the NTP antisense oligonucleotide

bound to the peptide, the peptidyl antisense agent is endocytosed and the NTP antisense oligonucleotide binds to the target NTP mRNA to inhibit translation (Haralambid *et al.*, WO 8903849; Lebleu *et al.*, EP 0263740).

5       The NTP antisense oligonucleotides and the pharmaceutical compositions of the present invention may be administered by any means that achieve their intended purpose. For example, administration may be by parenteral, subcutaneous, intravenous, intramuscular, intra-peritoneal, or transdermal routes. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of  
10       treatment, and the nature of the effect desired.

      Compositions within the scope of this invention include all compositions wherein the NTP antisense oligonucleotide is contained in an amount effective to achieve inhibition of proliferation and/or stimulate differentiation of the subject cancer cells, or alleviate AD. While individual needs vary,  
15       determination of optimal ranges of effective amounts of each component is with the skill of the art. Typically, the NTP antisense oligonucleotide may be administered to mammals, e.g. humans, at a dose of 0.005 to 1 mg/kg/day, or an equivalent amount of the pharmaceutically acceptable salt thereof, per day of the body weight of the mammal being treated.

20       Alternatively, antisense oligonucleotides can be prepared which are designed to interfere with transcription of the NTP gene by binding transcribed regions of duplex DNA (including introns, exons, or both) and forming triple helices (Froehler *et al.*, WO 91/06626; Toole, WO 92/10590). Preferred oligonucleotides for triple helix formation are oligonucleotides which have  
25       inverted polarities for at least two regions of the oligonucleotide (*Id.*). Such oligonucleotides comprise tandem sequences of opposite polarity such as 3'---5'-L-5'---3', or 5'---3'-L-3'---5', wherein L represents a 0-10 base oligonucleotide linkage between oligonucleotides. The inverted polarity form stabilizes single-stranded oligonucleotides to exonuclease degradation (Froehler  
30       *et al.*, *supra*). Preferred triple helix-forming oligonucleotides are based upon SEQ ID NOs 1-3:

1. 3'-TACTACCAGACAACCTTAGCC-5'-L-  
5'-CCGATTCCAACAGACCATCAT-3' [SEQ ID NO: 7];
2. 5'-CCGATTCCAACAGACCATCAT-3'-L-  
3'-TACTACCAGACAACCTTAGCC-5' [SEQ ID NO: 8];
- 5 3. 3'-CCACCTTACTACCAGACAACC-5'-L-  
5'-CCAACAGACCATCATTCCACC-3' [SEQ ID NO: 9];
4. 5'-CCAACAGACCATCATTCCACC-3'-L-  
3'-CCACCTTACTACCAGACAACC-5' [SEQ ID NO: 10];
5. 3'-CCAGACAACCTTAGCCAAACC-5'-L-  
10 5'-CCAAACCGATTCCAACAGACC-3' [SEQ ID NO: 11]; and
6. 5'-CCAAACCGATTCCAACAGACC-3'-L-  
3'-CCAGACAACCTTAGCCAAACC-5' [SEQ ID NO: 12].

Thus, triple helix-forming oligonucleotides 1 and 2 are represented as 3'[SEQ ID NO: 1]5'-L-5'[SEQ ID NO: 1]3' and 5'[SEQ ID NO: 1]3'-L-3'[SEQ ID NO: 1]5', respectively. Triple helix-forming oligonucleotides 3 and 4 are represented as 3'[SEQ ID NO: 2]5'-L-5'[SEQ ID NO: 2]3' and 5'[SEQ ID NO: 2]3'-L-3'[SEQ ID NO: 2]5', respectively. Triple helix-forming oligonucleotides 5 and 6 are represented as 3'[SEQ ID NO: 3]5'-L-5'[SEQ ID NO: 3]3' and 5'[SEQ ID NO: 3]3'-L-3'[SEQ ID NO: 3]5', respectively. Of course, similar triple helix-forming oligonucleotide may be prepared with SEQ ID NOs. 4-6, or fragments thereof.

In therapeutic application, the triple helix-forming oligonucleotides can be formulated in pharmaceutical preparations for a variety of modes of administration, including systemic or localized administration, as described above.

The antisense oligonucleotides of the present invention may be prepared according to any of the methods that are well known to those of ordinary skill in the art, as described above.

Ribozymes provide an alternative method to inhibit mRNA function. Ribozymes may be RNA enzymes, self-splicing RNAs, and self-cleaving RNAs (Cech *et al.*, *Journal of Biological Chemistry* 267:17479-17482 (1992)).

It is possible to construct *de novo* ribozymes which have an endonuclease activity directed in *trans* to a certain target sequence. Since these ribozymes can act on various sequences, ribozymes can be designed for virtually any RNA substrate. Thus, ribozymes are very flexible tools for inhibiting the expression of specific genes and provide an alternative to antisense constructs.

A ribozyme against chloramphenicol acetyltransferase mRNA has been successfully constructed (Haseloff *et al.*, *Nature* 334:585-591 (1988); Uhlenbeck *et al.*, *Nature* 328:596-600 (1987)). The ribozyme contains three structural domains: 1) a highly conserved region of nucleotides which flank the cleavage site in the 5' direction; 2) the highly conserved sequences contained in naturally occurring cleavage domains of ribozymes, forming a base-paired stem; and 3) the regions which flank the cleavage site on both sides and ensure the exact arrangement of the ribozyme in relation to the cleavage site and the cohesion of the substrate and enzyme. RNA enzymes constructed according to this model have already proved suitable *in vitro* for the specific cleaving of RNA sequences (Haseloff *et al.*, *supra*).

Alternatively, hairpin ribozymes may be used in which the active site is derived from the minus strand of the satellite RNA of tobacco ring spot virus (Hampel *et al.*, *Biochemistry* 28:4929-4933 (1989)). Recently, a hairpin ribozyme was designed which cleaves human immunodeficiency virus type 1 RNA (Ojwang *et al.*, *Proc. Natl. Acad. Sci. USA* 89:10802-10806 (1992)). Other self-cleaving RNA activities are associated with hepatitis delta virus (Kuo *et al.*, *J. Virol.* 62:4429-4444 (1988)).

As discussed above, preferred targets for NTP ribozymes are the nucleotide sequences which are not homologous with PTP sequences. Preferably, the NTP ribozyme molecule of the present invention is designed based upon the chloramphenicol acetyltransferase ribozyme or hairpin ribozymes, described above. Alternatively, NTP ribozyme molecules are designed as described by Eckstein *et al.* (International Publication No. WO 92/07065) who disclose catalytically active ribozyme constructions which have

increased stability against chemical and enzymatic degradation, and thus are useful as therapeutic agents.

In an alternative approach, an external guide sequence (EGS) can be constructed for directing the endogenous ribozyme, RNase P, to intracellular NTP mRNA, which is subsequently cleaved by the cellular ribozyme (Altman *et al.*, U.S. Patent No. 5,168,053). Preferably, the NTP EGS comprises a ten to fifteen nucleotide sequence complementary to an NTP mRNA and a 3'-NCCA nucleotide sequence, wherein N is preferably a purine (*Id.*). After NTP EGS molecules are delivered to cells, as described below, the molecules bind to the targeted NTP mRNA species by forming base pairs between the NTP mRNA and the complementary NTP EGS sequences, thus promoting cleavage of NTP mRNA by RNase P at the nucleotide at the 5' side of the base-paired region (*Id.*).

Included as well in the present invention are pharmaceutical compositions comprising an effective amount of at least one NTP ribozyme or NTP EGS of the invention in combination with a pharmaceutically acceptable carrier. Preferably, the NTP ribozyme or NTP EGS is coadministered with an agent which enhances the uptake of the ribozyme or NTP EGS molecule by the cells. For example, the NTP ribozyme or NTP EGS may be combined with a lipophilic cationic compound which may be in the form of liposomes, as described above. Alternatively, the NTP ribozyme or NTP EGS may be combined with a lipophilic carrier such as any one of a number of sterols including cholesterol, cholate and deoxycholic acid. A preferred sterol is cholesterol.

The NTP ribozyme or NTP EGS, and the pharmaceutical compositions of the present invention may be administered by any means that achieve their intended purpose. For example, administration may be by parenteral, subcutaneous, intravenous, intramuscular, intra-peritoneal, or transdermal routes. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. For example, as much as 700

milligrams of antisense oligodeoxynucleotide has been administered intravenously to a patient over a course of 10 days (i.e., 0.05 mg/kg/hour) without signs of toxicity (Sterling, "Systemic Antisense Treatment Reported," *Genetic Engineering News* 12(12):1, 28 (1992)).

5           Compositions within the scope of this invention include all compositions wherein the NTP ribozyme or NTP EGS is contained in an amount which is effective to achieve inhibition of proliferation and/or stimulate differentiation of the subject cancer cells, or alleviate AD. While individual needs vary, determination of optimal ranges of effective amounts of each  
10       component is with the skill of the art.

          In addition to administering the NTP antisense oligonucleotides, ribozymes, or NTP EGS as a raw chemical in solution, the therapeutic molecules may be administered as part of a pharmaceutical preparation containing suitable pharmaceutically acceptable carriers comprising excipients  
15       and auxiliaries which facilitate processing of the NTP antisense oligonucleotide, ribozyme, or NTP EGS into preparations which can be used pharmaceutically.

          Suitable formulations for parenteral administration include aqueous solutions of the NTP antisense oligonucleotides, ribozymes, NTP EGS in  
20       water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances which  
25       increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. Optionally, the suspension may also contain stabilizers.

          Alternatively, NTP antisense RNA molecules, NTP ribozymes, and NTP EGS can be coded by DNA constructs which are administered in the  
30       form of virions, which are preferably incapable of replicating *in vivo* (see, for example, Taylor, WO 92/06693). For example, such DNA constructs may be

administered using herpes-based viruses (Gage *et al.*, U.S. Patent No. 5,082,670). Alternatively, NTP antisense RNA sequences, NTP ribozymes, and NTP EGS can be coded by RNA constructs which are administered in the form of virions, such as retroviruses. The preparation of retroviral vectors is well known in the art (*see*, for example, Brown *et al.*, "Retroviral Vectors," in *DNA Cloning: A Practical Approach*, Volume 3, IRL Press, Washington, D.C. (1987)).

Specificity for gene expression in the central nervous system can be conferred by using appropriate cell-specific regulatory sequences, such as cell-specific enhancers and promoters. For example, such sequences include the sequences that regulate the oligodendroglial-specific expression of JC virus, glial-specific expression of the proteolipid protein, and the glial fibrillary acidic protein genes (Gage *et al.*, *supra*). Since protein phosphorylation is critical for neuronal regulation (Kennedy, "Second Messengers and Neuronal Function," in *An Introduction to Molecular Neurobiology*, Hall, Ed., Sinauer Associates, Inc. (1992)), protein kinase promoter sequences can be used to achieve sufficient levels of NTP gene expression.

Thus, gene therapy can be used to alleviate AD by inhibiting the inappropriate expression of a particular form of NTP. Moreover, gene therapy can be used to alleviate AD by providing the appropriate expression level of a particular form of NTP. In this case, particular NTP nucleic acid sequences may be coded by DNA or RNA constructs which are administered in the form of viruses, as described above. Alternatively, "donor cells" may be modified *in vitro* using viral or retroviral vectors containing NTP sequences, or using other well known techniques of introducing foreign DNA into cells (*see*, for example, Sambrook *et al.*, *supra*). Such donor cells include fibroblast cells, neuronal cells, glial cells, and connective tissue cells (Gage *et al.*, *supra*). Following genetic manipulation, the donor cells are grafted into the central nervous system and thus, the genetically-modified cells provide the therapeutic form of NTP (*Id.*).



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Moreover, such virions may be introduced into the blood stream for delivery to the brain. This is accomplished through the osmotic disruption of the blood brain barrier prior to administration of the virions (*see*, for example, Neuwelt, United States Patent No. 4,866,042). The blood brain barrier may be disrupted by administration of a pharmaceutically effective, nontoxic hypertonic solution, such as mannitol, arabinose, or glycerol (*Id.*).

The following clones in *E. coli* were deposited according to the Budapest Treaty with the American Type Culture Collection (12301 Parklawn Drive, Rockville, Maryland, 20852): G2-2 PstI-DH5 (ATCC No. 69257); G5d-PstI-DH5 (ATCC No. 69258); 1-9a-LX-1 blue (ATCC No. 69259); AD3-4-DH1 (ATCC No. 69260); HB4-XL-blue (ATCC No. 69261); AD10-7-DH1 (ATCC No. 69262); AD2-2-DH1- (ATCC No. 69263); G5d-1PstI-EcoRI-DH5 (ATCC No. 69264); and G2-2PstI-EcoRI-DH5 (ATCC No. 69265).

Having now generally described the invention, the same will be more readily understood through reference to the following Examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

### *Example 1*

#### *Expression of NTP Immunoreactivity in Cell Lines*

Seven cell lines of central nervous system origin were identified that express thread protein immunoreactivity using the Th9 monoclonal antibody which was generated to the pancreatic form of the protein (Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985)), but cross-reacts with thread proteins present in brain tissue and cerebrospinal fluid (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). Among them were the following: two primitive neuroectodermal tumor (PNET) cell lines designated PNET1 and PNET2; three glioblastoma cell lines Hgl 16, Hgl 17, and C6;

the A172 glial cell line; and the SH-Sy5y neuroblastoma cell line. The glioblastoma cell lines and the A172 cells were obtained from the American Type Culture Collection (ATCC). SH-Sy5y cells were obtained from Dr. Biedler at Sloan-Kettering Memorial Hospital. The PNET cell lines have been  
5 described previously (The *et al.*, *Nature genetics* 3:62-66 (1993)), and were obtained from Dr. Rene' Bernards at the MGH Cancer Center. All cell lines were maintained in Earl's Modified Eagle Medium supplemented with 10% fetal calf serum, and without antibiotics.

To examine the cells for thread protein and other immunoreactivities,  
10 the cultures were harvested in phosphate buffered saline (PBS) (137 mM NaCl, 2.7 mM KCl, 4.3 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.4 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.3) containing 2 mM EDTA, and cytospin preparations were made using 10<sup>5</sup> cells per slide. The cytospin preparations were fixed immediately in 100% methanol (-20°C), air-dried, and then stored at -80°C until used. Prior to immunostaining, the  
15 slides were equilibrated to room temperature and hydrated in PBS. Nonspecific antibody binding was blocked with 3% nonimmune horse serum. Replicate cytospin preparations from the same cultures were incubated overnight at 4°C with 5 or 10 µg/ml of primary antibody. Immunoreactivity was revealed by the avidin-biotin horseradish peroxidase method using the Vectastain Elite kit (Vector Laboratories, Burlingame, CA) according to the  
20 manufacturer's protocol, and with 3-3' diaminobenzidine (0.5 mg/ml plus 0.03% hydrogen peroxide) as the chromogen. The cells then were counterstained with hematoxylin, dehydrated in graded alcohol solutions, cleared in xylenes, and preserved under coverglass with Permount (Fisher Scientific).

Cytospin preparations of each cell line were immunostained with the thread protein monoclonal antibodies Th9, Th7, Th10, Th29, Th34, TH46, Th67, and Th90. In addition, replicate slides were immunostained with positive (neurofilament, glial fibrillary acidic protein (GFAP), and vimentin)  
30 and negative (desmin, Hepatitis B surface antigen-5C3) control monoclonal antibodies. Except for 5C3 which was generated in the inventor's laboratory

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(Fujita *et al.*, *Gastroenterology* 91:1357-1363 (1986)), the control antibodies were purchased (Boehringer-Mannheim). All serological reagents were diluted in PBS containing 1 % bovine serum albumin (BSA), and all incubations except the one with primary antibody were carried out at room temperature in humidified chambers. The slides were washed in 3 changes of PBS between each step.

Both PNET1 and PNET2 cells expressed high and middle molecular weight neurofilament proteins and little or no glial fibrillary acidic protein or vimentin. The PNET1, PNET2, and SH-Sy5y cells expressed GAP-43, an abundant calmodulin-binding phosphoprotein that is highly expressed in immature neurons and in neurons undergoing regenerative cell growth (Benowitz *et al.*, *J. Neurosci.* 3:2153-2163 (1983); DeGraan *et al.*, *Neurosci. Lett.* 61:235-241 (1985); Kalil *et al.*, *J. Neurosci.* 6:2563-2570 (1986)). The A172 and C6 cells expressed GFAP and vimentin. However, A172 also exhibited neurofilament immunoreactivity, raising doubt about its purely glial cell nature. None of the cell lines manifested immunoreactivity with monoclonal antibodies to desmin or to Hepatitis B surface antigen. As a negative control cell line, the Huh7 hepatocellular carcinoma cell line was similarly immunostained, and found not to exhibit any immunoreactivity with the above antibodies. However, the Huh cells were immunoreactive with monoclonal antibodies to the insulin receptor substrate protein, IRS-1 (data not shown) which was used as a positive control for this cell line (Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993)).

Using the Th9 monoclonal antibody, thread protein immunoreactivity was detected in primary PNET (A), primary glioblastoma (F), PNET1 (B), and C6 cells (G), but not in hepatocellular carcinoma cell lines (Figure 1). In addition, Th9 immunoreactivity was detected in histological sections from 8 of the 9 primary human CNS PNETs, and from all 5 of the primary human glioblastomas studied (Figure 1). Although all 5 cell lines exhibited intense immunoreactivity with the Th9 monoclonal antibody, they differed with respect to immunoreactivity for other Th monoclonal antibodies. The

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immunostaining reaction generated with the Th10 (C,H), Th7 (D,I), or Th46 monoclonal antibodies was either low-level (C,D) or absent (H,I,E,J) in PNET1 (C-E) and C6 (H-J). PNET2 cells exhibited only low levels of immunoreactivity with Th7 and Th29, and they manifested no immunostaining with the other Th monoclonal antibodies. A172, C6, and SH-Sy5y cells displayed little or no immunoreactivity with Th monoclonal antibodies other than Th9. Huh7 cells exhibited no immunoreactivity with any of the thread protein monoclonal antibodies employed, whereas human pancreatic tissue was immunoreactive with all of the Th antibodies, which had been generated against the purified pancreatic form of thread protein (Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985)).

### Example 2

#### *Analysis of Thread Proteins by Monoclonal Antibody-Based Immunoradiometric Assay (M-IRMA)*

Cultured cells were washed in PBS and recovered in PBS containing 2 mM EDTA. The cells were pelleted by centrifugation at 1000 x g for 15 min, and then resuspended in lysis buffer containing 50 mM Tris-HCl (pH 7.5), 1% Triton X-100, 2 mM EGTA, 10 mM EDTA, 100 mM NaF, 1 mM  $\text{Na}_4\text{P}_2\text{O}_7$ , 2 mM  $\text{Na}_3\text{VO}_4$ , 100  $\mu\text{g/ml}$  phenylmethylsulfonyl fluoride, 1  $\mu\text{g/ml}$  aprotinin, 1  $\mu\text{g/ml}$  pepstatin A, and 1  $\mu\text{g/ml}$  leupeptin. The supernatant fractions obtained by centrifugation of the lysates at 14,000 x g for 10 min were used for the Western blot analysis, immunoprecipitation studies, and M-IRMA. Protein concentration was determined by the Lowry colorimetric assay. The samples were stored at  $-40^\circ\text{C}$ .

M-IRMA is a highly sensitive two- or three-site forward sandwich assay which permits quantitation of picomolar NTP in cell lysates, tissue culture medium, tissue homogenates, and body fluids (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992);

de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992); Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985)). In addition, when combined with SDS-PAGE, M-IRMA can be used to determine molecular size of thread proteins and related species (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989);  
5 de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). M-IRMA involves capturing the immunoreactive thread proteins present in biological samples using monoclonal antibodies Th7 and Th10 affixed to a solid-phase matrix, and then detecting the captured antigen with  
10 a third radiolabeled tracer monoclonal antibody (Th9) to the same protein. Briefly, 1/4" polystyrene beads (Precision Ball, Inc) were coated with one or two monoclonal antibodies to thread proteins (usually Th7 + Th10). Cell lysates or supernatant fractions of tissue homogenates (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.*  
15 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)) were incubated over night with the coated beads to capture thread proteins present in the samples. The beads were washed 5x in PBS, and then incubated with <sup>125</sup>I labeled Th9 as a tracer to detect the captured thread proteins. The concentration of thread  
20 protein in the lysate or tissue homogenate was determined from a standard curve generated with known quantities of purified thread protein. This highly sensitive assay can detect as little as 10 pmol of thread protein in solution. To assay for thread proteins fractionated by SDS-PAGE, the wet gels were sliced at 2 mm intervals, and the proteins were eluted from each fraction into 0.5 ml  
25 of PBS by shaking for 24 hours at room temperature. The eluates were assayed directly for thread proteins by M-IRMA.

Corresponding with the widespread immunocytochemical staining of PNET1 cells with Th7, Th10, Th34, and Th29, thread protein immunoreactivity was readily measured in these cells by M-IRMA. In other  
30 words, with Th7, Th10, Th34, and Th29 monoclonal antibodies (MoAb) used as capture antibodies, either singularly or with two of them together, and <sup>125</sup>I

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labeled Th9 was used as the tracer, similarly high levels of thread protein were measured (Figure 2). In contrast, in PNET2, C6, and A172 cells, which exhibited intense immunoreactivity with Th9, but little or no immunocytochemical staining with the Th monoclonal antibodies that were used to capture antigen, the levels of thread protein detected by M-IRMA were much lower than those measured in the PNET1 cells (Figure 2). Similarly, Huh7 cells, which manifested no immunocytochemical staining with any of the thread protein monoclonal antibodies, had virtually nondetectable levels of thread proteins in the cellular lysates by M-IRMA. The concentrations of thread protein in the cell lysates were computed from a standard curve generated with purified PTP using Th7 and Th10 as capture antibodies. The results expressed as mean S.D. pg/mg of total protein were as follows: PNET1-13.1  $\pm$  0.39; PNET2-2.06  $\pm$  0.10; A172-3.38  $\pm$  0.37; C6-2.52  $\pm$  0.22; and Huh7-0.34  $\pm$  0.05.

### Example 3

#### *Characterization of Neural Thread Proteins in Tumor Cell Lines*

In Western Blot analysis, samples containing 100  $\mu$ g of protein were fractionated by SDS-PAGE, along with pre-labeled molecular weight standards. The proteins were blotted onto nylon membranes (Immobilon-P transfer membrane, Millipore) using a semi-dry transfer apparatus (Integrated Systems). The membranes were washed in Tris buffered saline (TBS; 10 mM Tris, 0.85 % sodium chloride, pH 7.5), and then blocked with TBS containing 3% BSA. The blots were incubated overnight at 4°C with  $^{125}$ I labeled Th9 monoclonal antibody. Unspecifically bound probe was removed by washing the membranes at room temperature in TBS-BSA 3 x 15 min. and 1 x 30 min. The results were analyzed by autoradiography using Kodak XAR film.

To prepare samples for immunoprecipitation studies, one milliliter samples of cell lysate containing approximately 1 mg/ml of protein were used for immunoprecipitation studies. The lysates were initially pre-cleared with non-relevant antibody (5C3 or antidesmin), and then with Protein A sepharose. Thread proteins were immunoprecipitated using 5-10  $\mu$ g of Th9 and Protein A sepharose (Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993)). The immune complexes collected by centrifugation were resuspended in buffer containing 2% SDS and 10 mM  $\beta$ -mercaptoethanol, and then subjected to SDS-PAGE under denaturing and reducing conditions (*Id.*). Crude cellular lysates (100  $\mu$ g protein) were analyzed simultaneously. The proteins were blotted onto Immobilon-P membranes and probed with  $^{125}$ -I labeled (*Id.*) Th9 to detect thread proteins and related molecules. Negative control experiments were performed simultaneously using either monoclonal antibodies to Hepatitis B surface antigen (5C3) or to desmin.

Metabolic labeling experiments were performed using monolayers of cells cultured in 100 mm<sup>2</sup> petri dishes. Prior to labeling, the cells were exposed to methionine- and cysteine-free medium for 2 h. The medium was then replaced with 3 ml of DMEM containing 300  $\mu$ Ci each of [ $^{35}$ S] methionine or [ $^{35}$ S] cysteine. After labeling for 3 hours, the cells were incubated for various intervals with complete medium devoid radiolabeled amino acids and supplemented with 10 mM methionine. Cell lysates were prepared as described above. Thread proteins were immunoprecipitated using the Th9 monoclonal antibody and protein A sepharose, and the immunoprecipitation products were analyzed by SDS-PAGE and film autoradiography.

For the *in vivo* phosphorylation studies, cells cultured as described for metabolic labeling studies were washed twice with TBS and incubated for 2 h with phosphate-free Dulbecco's MEM containing 10% dialyzed fetal calf serum. Then the cells were washed with TBS and incubated for 3 h with the same medium containing 400  $\mu$ Ci/ml of [ $^{32}$ P] orthophosphoric acid. The cell lysates were analyzed by immunoprecipitation with thread protein, and both

positive (p36) and negative (desmin) control monoclonal antibodies, followed by SDS-PAGE.

In order to study the glycosylation state of neural thread proteins, cell culture lysates containing approximately 100  $\mu$ g of protein were subjected to SDS-PAGE, and the fractionated proteins were transferred to Immobilon-P membranes (Millipore). O- and N-glycans were detected by periodate oxidation followed by biotinylation, and then Western blot analysis with a Streptavidin-alkaline phosphatase probe and NBT/BCIP as the colorimetric substrate. The assays were performed using the GlycoTrack Kit (Oxford Glycosystems, Rosedale, NY) according to the protocol provided by the manufacturer.

Th9-immunoreactive proteins were detected in lysates of PNET1, PNET2, SH-Sy5y, C6, and A172 cells by four different methods: Western blot analysis, immunoprecipitation followed by Western blot analysis, metabolic labeling followed by immunoprecipitation, and SDS-PAGE combined with M-IRMA. Western blot analysis of crude cellular lysates using  $^{125}$ I-labeled Th9 demonstrated ~21 kDa bands in the above cell lines (as indicated by the arrow in Figure 3), but the signal intensity was low. In contrast, in lysates of human pancreatic tissue, the expected 17 kDa uncleaved and 14 kDa cleaved forms of pancreatic thread protein were readily detected by Western blot analysis (Figure 3). Thread proteins were not detected in lysates of human hepatocellular carcinoma cell lines. The strikingly greater abundance of thread proteins in pancreatic tissue compared with neuronal and glial cell lines is consistent with a previous finding of  $10^6$ -fold higher levels of thread proteins in pancreas and pancreatic juice compared with brain tissue and cerebrospinal fluid (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). Although one would expect that thread proteins synthesized by PNET and glial cells are secreted as is the case for PTP and NTP, thread proteins



were not detected in the tissue culture medium by Western blot analysis, even after concentrating the medium four- or five-fold by lyophilization.

Th9-immunoreactive thread proteins were more readily detected in PNET and glial cell lines by first immunoprecipitating from the lysates with either Th7+Th10 or Th9, and then performing Western blot analysis using <sup>125</sup>I-labeled Th9 (direct) (Figure 3), or unlabeled Th9 with <sup>125</sup>I-labeled Protein A (indirect). Both methods demonstrated 21 kDa thread protein-related species, similar to those detected by Western blot analysis. In addition, ~17 kDa bands were also observed in both PNET and glial cells, but the signal was inconsistent and low-level, as determined by Western blot analysis. As negative controls, the Huh7, HepG2, and FOCUS (Lun *et al.*, *In Vitro* (Rockville) 20:493-504 (1984)) human hepatocellular carcinoma cell lines were studied simultaneously under identical conditions, and Th9-immunoreactive proteins were not detected in the cellular lysates.

The molecular sizes of thread proteins present in PNET and glial cells were most prominently demonstrated by metabolic labeling with <sup>35</sup>S-methionine or <sup>35</sup>S-cysteine, followed by immunoprecipitation using Th9 monoclonal antibody. Monoclonal antibodies to desmin or to hepatitis B surface antigen (5C3) were used as negative controls for immunoprecipitation. In both PNET and glial cell lines, ~26 and ~21 kDa Th9-immunoreactive proteins were detected by SDS-PAGE analysis of the immunoprecipitated products (Figure 4, right panel). In PNET1 cells, the 21 kDa band appeared as a doublet (left panel); the accompanying slightly higher molecular weight species appeared to be less abundant than the dominant band at ~21 kDa. In addition, in both PNET and glial cell lines, there were also ~17 kDa Th9-immunoreactive proteins associated with bands of nearly the same intensity as the ~21 kDa bands. In C6 cells, there were also ~26 kDa, ~14-15 kDa and ~8 kDa Th9-immunoreactive proteins which were not detected in PNET cells (Figure 4, arrows).

The 21 kDa and 17 kDa thread proteins in SH-Sy5y, PNET1, A172, and C6 cells, and their absence in hepatocellular carcinoma cells were also

demonstrated by SDS-PAGE/M-IRMA (Figure 5). Cellular proteins fractionated by SDS-PAGE were eluted from the gels sliced at 2 mm intervals, and assayed directly for thread protein immunoreactivity by M-IRMA using Th7+Th10 as capture antibodies, and  $^{125}\text{I}$ -labeled Th9 as the tracer. Despite low levels, two distinct peaks were evident in all neuroectodermal cell lines, but not in Huh7 hepatocellular carcinoma cells assayed simultaneously and in the same manner. The resolution of these gels did not permit distinction of ~17 kDa from ~14-15 kDa proteins which might have been present.

PNET1 and C6 cells were metabolically labeled with  $^{32}\text{P}$  or  $^{35}\text{S}$ -methionine, and thread proteins were immunoprecipitated from the lysates using Th9 monoclonal antibody (Figure 6). As a negative control, immunoprecipitation studies were conducted using an equal portion of the cellular lysate and monoclonal antibodies to desmin protein (Figure 6, right panel). In the cells labeled with  $^{35}\text{S}$  methionine, Th9-immunoreactive bands were detected at ~26 kDa and ~21 kDa (upper arrows), ~17 kDa (lower arrows), and also at ~14-15 kDa (Figure 6). After  $^{32}\text{P}$  labeling, only the 21 kDa band was observed by immunoprecipitation with Th9 monoclonal antibody; the other molecular weight species did not appear to be phosphorylated (Figure 6). Phosphorylated Th9-immunoreactive proteins were detected in C6 cells, but not in PNET1 cells, but this might be due to less efficient labeling since PNET1 cells grow slower than C6 cells. No bands in the 14 kDa to 26 kDa range were detected using monoclonal antibodies to desmin for immunoprecipitation (Figure 6). Carbohydrate moieties were not detected in Th9 immunoprecipitated proteins (data not shown).

The highest concentrations of thread protein were measured in subconfluent cultures of PNET1 cells, i.e. during the log phase of growth, and the lowest concentrations in overnight serum-starved cultures (growth arrest) (Figure 7). Cultures that were 100% confluent also had lower levels of thread protein expression compared with proliferating cultures. Huh7 hepatocellular carcinoma cells (negative control) were simultaneously studied using identical culture conditions, but the levels of thread protein remained low throughout.

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Surprisingly, there was no change in the degree of thread protein immunocytochemical staining of PNET cells cultured under these various conditions. However, the degree to which the levels of thread proteins changed by M-IRMA measurement may not have been detectable by immunocytochemistry. Nevertheless, the reduction in cellular thread protein content induced by serum starvation was associated with a change in the phenotype of the cells. When the cells achieved 100% confluence or after they had been subjected to overnight serum starvation, the cell bodies reduced in size, and they exhibited striking changes in the degree and distribution of immunoreactivity for neurofilament protein, GAP-43, and GFAP (Figure 8). In PNET cultures that were 50% confluent, the cells exhibited punctate and often a polar distribution of neurofilament and GAP-43 immunoreactivity, whereas 100% confluent and serum-starved PNET cultures exhibited diffuse perikaryal immunoreactivity for both neurofilament and GAP-43. The punctate immunoreactivity may have corresponded with distribution of neurofilament and GAP-43 in neurites. In contrast, 50% confluent PNET cultures were devoid of GFAP immunoreactivity, while 100% confluent and serum-starved cultures contained conspicuous proportions of GFAP-positive cells. Moreover, the proportion of GFAP-immunoreactive cells was greatest in 100% confluent serum-starved cultures, followed by 50% confluent serum-starved cultures, and then 100% confluent cultures with medium containing 10% fetal calf serum. Therefore, the reduction in thread protein levels measured in PNET cells subjected to overnight serum starvation may have been due to differentiation of the cells toward an astrocytic phenotype. C6 cells and other glioblastoma cell lines exhibited intense immunoreactivity with the Th9 monoclonal antibody, but the levels of thread protein measured by M-IRMA were often low, possibly due to low-level immunoreactivity with other thread protein antibodies, including Th7 and TH10 (see Figure 1).

### Example 4

#### *Cloning of Thread Proteins from Human cDNA Libraries*

Human brain cDNA libraries made from 17-18 week old fetal brain (Stratagene, Inc., La Jolla, CA), 2 year-old temporal lobe neocortex (Stratagene), and end-stage Alzheimer's disease cerebral cortex (In Vitrogen; San Diego, CA) were screened using probes generated from a 416 bp DNA fragment corresponding to nucleotides 235-650 of the rat PTP cDNA. The rat PTP cDNA, designated O18, was isolated from a rat pancreatic cDNA library using synthetic 60mer DNA probes corresponding to nucleotides 45-104 and 345-404 of the published sequence (Terazono *et al.*, *J. Biol. Chem.* 263:2111-2114 (1988); Watanabe *et al.*, *J. Biol. Chem.* 265:7432-7439 (1990)). Approximately  $2 \times 10^6$  plaques or colonies from each library were screened with low-stringency hybridization using standard techniques (*see* Sambrook *et al.*, *supra*). Putative clones were plaque/colony purified, and the DNA inserts were sequenced by the dideoxynucleotide chain termination method using T7 polymerase (USB Sequenase; United States Biochemical Corp., Cleveland, OH). The sequences were compared with the Genbank database, and aligned with the nucleic acid sequences of other thread protein cDNAs.

#### *1. CNS Neural Thread Protein cDNA Isolated from Human Fetal Brain Library*

A 1.35 kilobase (kb) 1-9a CNS thread protein partial cDNA was isolated in which only a small segment corresponds to an open reading frame, and the remainder, to a 3' untranslated region (Figure 9a). The sequence of an additional 150 nucleotides was obtained from 5' anchor PCR amplification products. A second round of 5' anchor PCR amplification yielded a further upstream 600 bp product (Figure 9b). A portion of the 1-9a cDNA sequence shares significant homology with the 5' end of the human PTP cDNA and the Reg gene (Figure 10a). In addition, the initial 5' anchor PCR product has

60% homology with the 5' end of the Reg gene, and 63% homology with Exon 2 of the human Reg gene (Figure 10b). Moreover, probes generated from the 590 bp 5'-end fragment of 1-9a cDNA hybridized with human brain and pancreas mRNA (Figure 12). The 1-9a sequence is also homologous with the AD2-2 and AD3-4 cDNAs in that at one end of their completed sequences, the overlaps are substantial (Figure 10c).

2. *CNS Neural Thread Protein cDNA Isolated from a Two-Year Old Temporal Cortex Library*

The HB4 clone is a 593 base pair partial cDNA that was isolated from a 2-year old temporal cortex library. This cDNA contains an open reading frame at its 5' end and terminates at nucleotide 275. There is a polyadenylation signal beginning at nucleotide 475, and the sequence ends with a poly-A tail (Figure 11a). The deduced amino acid sequence of the partial HB4 clone predicts a protein with a molecular weight of 10.4 kDa, and a pI of 12.1. The HB4 cDNA exhibits 50% overall nucleic acid homology with the human PTP cDNA (Figure 11b), a segment of the human Reg gene (Figure 11c).

3. *Isolation of Neural Thread Protein cDNAs from an Alzheimer's Disease Library*

Using the O18 rat PTP cDNA probe, four related cDNAs were isolated from an AD brain library. These clones were designated: AD 2-2, AD 3-4, AD 4-4 and AD 16c (also called AD 10-7) (Figures 16a-16l).

The AD 2-2 cDNA is approximately 1.2 kb and it shares significant homology with the 1-9a cDNA, AD 16c, rat PTP cDNA, and Exon 1 of the human Reg gene (Figure 17). The AD 2-2 probe generates a genomic Southern blot pattern similar to that obtained with the AD 3-4 probe. Figure 16b depicts the complete nucleotide sequence of the AD2-2 cDNA clone that

was isolated from an AD brain library. Random primer generated probes based on this sequence hybridized with human brain and neuronal samples but not with glial cell lines or with pancreatic RNA.

Figures 16c, 16d, 16e and 16f depict partial nucleotide sequences of the AD3-4 cDNA clones that were isolated from an AD brain library. Random primer generated AD3-4 probes yielded two mRNA transcripts, 1.6 kB and 3.4 kB. These mRNA species are over-expressed in AD brains, with an average of two-fold elevation compared with aged matched controls (N=8).

The AD 3-4 cDNA 1.6 kb clone is identical to another clone isolated at the same time (AD 5-3) (Figure 18a). The AD 3-4/AD 5-3 cDNA exhibits substantial homology with the 1-9a 5' anchor PCR products (Figure 18b), as well as with the human Reg gene and the Gen2a-EP genomic clone (Figure 18c). Southern blot analysis of human genomic DNA with the AD 3-4 probe revealed a pattern similar to that obtained with the AD 2-2 probe.

Figures 16g and 16h depict the partial nucleotide sequence of AD 4-4 which is a 0.8 kb partial cDNA clone which is identical to another cDNA isolated at the same time (AD 3-5). This AD 4-4 clone shares substantial sequence homology with AD 2-2 and 1-9a cDNAs (Figure 19). Figure 16i depicts the complete nucleotide sequence of a partial cDNA clone isolated from an AD brain library. This cDNA hybridized with brain and neuronal cell line mRNA, yielding a single 1.4 kB transcript.

Figure 16j depicts the nucleotide sequence of the 0.5 kb partial cDNA clone AD 16c (also called AD 10-7) that is 72% homologous with AD 2-2, and also aligns with human PTP and the human Reg gene sequences (Figures 20a and b).

Figure 16k depicts the complete nucleotide sequence of the AD10-7 clone that was isolated from an AD brain library. Hybridization of Northern blots using either antisense cRNA probes or random primer generated DNA probes detected 2.6, 1.9, 1.4 and 0.9 kB mRNA transcripts in neuronal cells. Neuronal cell lines expressed only the two largest transcripts, while mature adult human brains expressed predominantly the two smallest transcripts, and

either very low or nondetectable levels of the 2.6 kB and 1.9 kB transcripts. Using an AD10-7 probe, Northern blot analysis of RNA obtained from human liver, ovary, fallopian tube, colon, stomach, spleen, rectum, thyroid, 12 week placenta and kidney was negative.

5           Figure 16l depicts the complete nucleotide sequence of the AD16c cDNA clone that was isolated from an AD brain library. Hybridization of Northern blots using random primer generated DNA probes yielded the same results as obtained with the AD10-7 cDNA clone. The AD16c clone shares a 650 bp segment of near identity with AD10-7. In addition, elevated levels  
10 of AD16c mRNA were detected in AD brains compared with aged control brains by Northern blot analysis.

### Example 5

#### *Analysis of Brain Thread Protein Gene Expression*

Thread protein mRNA expression was examined in the following neuroectodermal tumor derived cell lines: central nervous system primitive neuroectodermal tumor cells designated PNET1 and PNET2; HGL-16 and HGL-17 human glioblastoma cells; A172 human glioma cells; C6 rat glioma cells; and SH-Sy5y neuroblastoma cells. In addition, human brain tissue from patients with Alzheimer's disease or no neurological disease (aged controls), and embryonic and postnatally developing rat brain were assayed for thread protein mRNA expression. RNA extracted from human and rat pancreas served as positive controls.

RNA was extracted in 5 M guanidinium isothiocyanate, and then isolated by centrifugation through a cesium chloride step gradient (*see Sambrook et al., supra*). RNA was quantified by measuring the absorbance at 260 nm and 280 nm. The thread protein mRNA transcript sizes were assessed by northern blot analysis, and the levels of expression were evaluated by RNA dot blot hybridization. Northern blot analysis was performed by electrophoresing samples containing 15  $\mu$ g of total cellular RNA through 1% agarose-formaldehyde gels. The RNA was transferred to nylon membrane, cross-linked with ultraviolet light, and hybridized with probes generated from a 600 bp fragment of the 1-9A cDNA clone. The fragment used for hybridization studies contained the regions most homologous with the human PTP cDNA. The probes were labeled with [ $^{32}$ P]  $\alpha$ -dCTP by the random primer method (Amersham Corporation; Arlington Heights, IL). The blots were hybridized overnight at 42°C with  $2 \times 10^6$  dpm /ml of probe in buffer containing 50% formamide, 5x SSPE, 10x Denhardt's (100x Denhardt's is 2% Ficoll, 2% bovine serum albumin, 2% polyvinylpyrrolidone), 0.5% SDS (sodium dodecyl sulfate), and 100  $\mu$ g/ml of sheared denatured salmon sperm DNA. The membranes were washed in SSPE containing 0.25% SDS using



standard methods. Autoradiograms were generated by exposing the membranes to Kodak XAR film at -80°C. The membranes were subsequently stripped of probe and then rehybridized with a synthetic 30mer corresponding to 18s RNA to evaluate sample loading.

5 Northern analysis of total cellular RNA using probes made from the 1-9a cDNA disclosed two dominant transcripts in central nervous system (CNS) tumor cell lines: one transcript was 1.6 kb, and the other was 0.9 kb (Figure 12A). In addition, in the SH-Sy5y neuroblastoma and PNET1 cell lines, a larger 4.2 kb mRNA transcript was also detected. The 4.2 kb transcript may  
10 represent preprocessed mRNA. The same size transcripts were detected in adult (R. Brain) and newborn (NB) rat, but the 0.9 kb transcript was more abundant in the adult brain whereas the 1.6 kb transcript was more abundant in the newborn rat brain. In rat pancreas (R. Panc.), only a 0.9 kb transcript was detected, corresponding to the size of rat PTP mRNA (Terazono *et al.*,  
15 *J. Biol. Chem.* 263:2111-2114 (1988); Watanabe *et al.*, *J. Biol. Chem.* 265:7432-7439 (1990)). mRNA transcripts were not detected in normal liver (NI Liver). Using a probe generated from the 3' region of the 1-9a cDNA, the 1.6 kb, but not the 0.9 kb transcript was revealed (Figure 12b). Using a 30-mer probe corresponding to the most 5'-end of the 1-9a cDNA, the higher  
20 molecular weight mRNA transcripts were detected (Figure 12c). The 0.9 kb transcript was also evident with longer exposure of the blot.

Northern analysis of human brain RNA disclosed a dominant 1.6 kb transcript, but also two and sometimes three smaller transcripts of 1.2 kb, 0.9 kb, and 0.8 kb (Figure 13, bottom). In contrast to the findings in cell lines,  
25 the 4.2 kb mRNA transcript was seldom observed in adult human brain. Hybridization with human pancreas disclosed a 0.8 kb transcript, corresponding with the size of PTP mRNA. The transcripts detected in human brain and pancreas using 1-9a probes were identical in size to the transcripts observed using PTP cDNA probes.

30 Dot blot RNA hybridization to 5 µg of total RNA using the 600 bp fragment of the 1-9a cDNA (NTP) demonstrated higher levels of expression

in AD, compared with aged control brains (Figure 13, top). Rehybridization of the same membrane with a cDNA corresponding to  $\beta$ -actin demonstrated similar loading of RNA in each dot. The observation of elevated levels of 1-9a-related mRNA in AD brain tissue is similar to that reported previously using 60mer probes corresponding to human PTP cDNA (de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990)). The differences between AD and control brains appeared to be due to differences in the levels of the 1.6 kb, 0.9 kb and 0.8 kb transcripts, as shown in Figure 13.

The AD-NTP 3-4 cDNA, isolated from the AD library, hybridizes with RNA from neuronal-derived neuroectodermal tumor cell lines, and human brain tissue. In the cell lines, 1.6 kb and 0.9 kb transcripts as observed with the 1-9a probe were detected (Figure 21c). However, in human brain, ~4 kb, 1.6 kb, and 0.9 kb transcripts were detected, and the levels of expression for all three transcripts were higher in AD compared with aged control brains (Figure 21d).

AD 4-4 cDNA probe hybridized only with a 0.9 kb transcript, and only in neuronal cell lines.

### Example 6

#### ***Direct Cloning and Sequencing of Thread Protein cDNAs from Neuroectodermal Tumor Cell Lines and Alzheimer's Disease Brain***

Thread protein cDNAs were cloned directly from PNET1, PNET2, SH-Sy5y, and A172 cells, and from Alzheimer's disease and aged control brain RNA using the 3'- and 5'-RACE methods (Frohman *et al.*, *Proc. Natl. Acad. Sci. USA* 85:8998 (1988); Ohara *et al.*, *Proc. Natl. Acad. Sci. USA* 86:5673 (1989); Loh *et al.*, *Science* 243:217 (1989)). Briefly, RNA was reverse transcribed using oligo-dT primers. For the 5'-RACE reaction, the cDNAs were amplified by polymerase chain reaction (PCR) using a specific 17-mer corresponding to a 5'-region of the 1-9a sequence, and a 17 dT

primer. The resulting PCR products were subjected to another round of amplification using another internal but overlapping 5'-end primer, and a specific 3'-17-mer corresponding to a 3' region of the 1-9a sequence. For the 3'-RACE reactions, the cDNAs were first tailed with dCTP using terminal deoxynucleotide transferase, and then they were amplified using a specific 17-mer corresponding to nucleotides 781-797 of the 1-9a clone and dG (17mer). A second nested PCR amplification was performed using a specific 17mer corresponding to nucleotides 766-792 at the 3' end, and dGTP (17mer) for the 5' end. The PCR products were subjected to Southern blot analysis using probes generated from an internal DNA fragment of the 1-9a cDNA clone, and from the O18 rat PTP cDNA clone. The PCR products were gel purified and ligated into pAmpl vectors using uracil deoxytransferase. The subcloned DNA inserts were sequenced by the dideoxynucleotide chain termination method using T7 DNA polymerase.

CNS thread protein transcripts were detected in neuroectodermal tumor cell lines and in AD human brain tissue by reverse transcription followed by PCR using specific primers corresponding to the 5' and 3' regions of the 1-9a cDNA sequence. Southern blot analysis of the PCR products demonstrated two dominant cross-hybridizing species, 0.8 kb and 1.0 kb (Figures 14a and 14b). In addition, in the SH-Sy5y cells, a larger 1.8 kb PCR product was also detected. In the PNET1, PNET2, SH-Sy5y, and A172 cells, a 0.4 kb PCR product that hybridized with the 1-9a probe was observed. Corresponding with the higher levels of thread protein mRNAs in Alzheimer's disease brains, the hybridization signal was more intense in AD samples compared with aged control samples.

The PCR products generated from the SH-Sy5y cells were subcloned and sequenced. Southern analysis of the cloned fragments exhibited intense hybridization with the 1-9a cDNA, and less intense but definite hybridization with the O18 cDNA (rat PTP) (Figure 14c). The nucleic acid sequence of the SH-Sy5y PCR clone (Sy-NTP) was identical to the 1-9a cDNA sequence.

### Example 7

#### *Isolation of Genomic Clones Coding for Human Brain Thread Proteins*

5 A human genomic DNA library was screened using probes made with a 600 bp fragment of the 1-9a human brain thread protein cDNA that was isolated from the two year-old temporal cortex library. The 1-9a cDNA fragment contained a region with 60% nucleic acid sequence homology with human PTP. After colony purification, the putative genomic clones were checked for cross-hybridization with the O18 rat PTP cDNA fragment.  
10 *EcoRI*, *PstI*, and *EcoRI/PstI* restriction fragments that hybridized with both the 1-9a and O18 probes were subcloned into pBluescript II vectors (Promega, Inc., Madison, WI) and then sequenced by the dideoxynucleotide chain termination method using either T7 polymerase (USB Sequenase) or polymerase chain reaction amplification and Vent polymerase.

15 Four genomic fragments designated G2-2 *PstI*, G2-2 *PstI-EcoRI*, G5d-1 *PstI*, and G5d-1 *PstI-EcoRI* were isolated from a human genomic DNA library (Figures 22a-22d). These genomic fragments all hybridized with both the 1-9a and O18 cDNA probes, and they ranged in size between 1.5 kb and 3 kb. Partial nucleic acid sequence information demonstrated homology between G2-  
20 2*PstI* and the human Reg gene and human and rat PTP cDNAs (Figure 23a); between G2-2 *PstI-EcoRI* and both the Reg gene and rat PTP cDNA (Figure 23b), and also with AD 2-2, AD 3-4, and the 1-9a cDNAs (data not shown); between G5d-1 *PstI* and the Reg gene and human PTP (Figure 23c); and between G5d-1 *PstI-EcoRI* and Reg gene, human PTP, 1-9a, and AD 4-4.

### Example 8

#### *In vitro Expression of the LacZ Fusion Protein and Demonstration of its Relatedness to Thread Proteins*

Fusion protein expression in bacteria containing the 1-9a cDNA clone, or one of the four genomic clones was induced with isopropylthio- $\beta$ -D-galactoside (IPTG) using standard techniques (Sambrook *et al.*, *supra*). Crude bacterial lysates from induced and uninduced cultures were subjected to SDS-PAGE and Western blot analysis using the Th9 monoclonal antibody to thread protein (Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993)), and  $^{125}$ -I labeled protein A to detect the bound antibody. In addition, bacterial lawns containing cloned DNA were induced to express the fusion protein with IPTG, and replica filters were probed directly with Th9 monoclonal antibody followed by  $^{125}$ -I labeled protein A.

Thread protein immunoreactivity was demonstrated in the bacterial fusion proteins by direct antibody binding to the IPTG-induced colonies (Figure 24). Thread protein immunoreactivity was detected using a cocktail of Th9, Th7, and Th10 monoclonal antibodies to PTP (Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993)), and  $^{125}$ -I labeled Protein A.

### Example 9

#### *Relative Levels of AD16c mRNA in AD and Aged Control Brains*

Northern blot analysis was performed using an AD16 cDNA probe. The blots were re-probed to detect 18s ribosomal RNA to evaluate loading of RNA in each lane. The unsaturated autoradiograms were subjected to densitometric analysis using a Molecular Dynamics Image Analyzer. The ratios of the AD16c and 18s RNA hybridization signals were plotted for each case, and the results are depicted graphically in Figure 25. The mean ratios (relative levels of AD16c) with standard errors are depicted in the smaller

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right hand graph. The findings confirm that there are elevated levels of AD16c mRNA expression in 6 of 9 AD brains compared to 1 of 6 age-matched controls. The difference between the mean levels is highly statistically significant ( $P < 0.005$ ). Similar results were obtained using AD10-7 probes. These results demonstrate that there is a statistically significant increase in levels of expression in AD brains compared to control brains.

### *Example 10*

#### *Preparation of Recombinant AD10-7 Fusion Protein and Detection Thereof With Monoclonal Antibodies*

AD10-7 cDNA was ligated into pTrcHIS vectors (In Vitrogen, San Diego) in three different reading frames (two incorrect-A and B, and one correct-C). Bacteria transformed with one of the three plasmids were induced with IPTG and bacterial lysates were examined for protein expression 0, 1 and 5 hours later. The proteins were fractionated by SDS-PAGE, and Western blot analysis was performed using monoclonal antibodies against the expressed tag protein (T7-tag mouse monoclonal antibodies; Novogen). The blots were developed using the avidin-biotin, horseradish peroxidase method, with diaminobenzidine as the chromogen (Figure 26). A band corresponding to ~45 kDA was detected in bacteria that had been transformed with plasmid DNA which contained AD10-7 ligated only in the correct reading frame (C) (arrow). The same size protein was observed by *in vitro* translation of the AD10-7 cDNA in a rabbit reticulocyte lysate assay system. In both systems, the fusion partner peptide was ~3 kDA, indicating that the cDNA encodes a protein of about ~42 kDA. A ~42 kDA NPT species is routinely detected by Western Blot analysis of neuronal cell lines and of human brain tissue.

### Example 11

#### *Demonstration of Neuronal Localization of AD10-7 mRNA Expression by In Situ Hybridization*

Sense and antisense cRNA probes were generated from linearized  
5 AD10-7 plasmid DNA using SP6 or T7 DNA-dependent RNA polymerase,  
respectively. The antisense probes hybridized with neuronal cell line mRNA  
as described above for this clone. The cRNA sense probes, on the other hand,  
failed to hybridize with RNA by Northern blot analysis. cRNA probes labeled  
with digoxigenin-UTP were hybridized with human brain tissue sections from  
10 early AD. After washing the sections extensively (de la Monte *et al.*, *J. Clin.  
Invest.* 86:1004-1013 (1990)), the hybridized probes were detected using  
peroxidase or alkaline phosphatase conjugated monoclonal antibodies to  
digoxigenin, and the colorimetric reactions were revealed using standard  
methods. Examination of the sections by brightfield and darkfield microscopy  
15 demonstrated hybridization of AD10-7 only in neurons (Fig. 27; dense  
aggregates of white grains over cell bodies in (A)). In contrast, and similar  
to the findings by Northern blot analysis, the *sense* AD10-7 cRNA probes  
failed to hybridize with brain tissue (B).

Although the foregoing refers to particular preferred embodiments, it  
20 will be understood that the present invention is not so limited. It will occur  
to those of ordinary skill in the art that various modifications may be made to  
the disclosed embodiments and that such modifications are intended to be  
within the scope of the present invention, which is defined by the following  
Claims.

25 All publications and patent applications mentioned in this specification  
are indicative of the level of skill of those in the art to which the invention  
pertains. All publications and patent applications are herein incorporated by  
reference to the same extent as if each individual publication or patent

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application was specifically and individually indicated to be incorporated by reference in their entirety.



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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>9</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69257
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: G2-2PstI-DH5	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

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A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>10</u>	
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Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69258
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: G5d-PstI-DH5	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69259
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: 1-9a-LX-1 blue	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

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B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input checked="" type="checkbox"/></span>	
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Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69260
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
Escherichia coli: AD3-4-DH1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69261
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: HB4-XL-blue	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
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Date of deposit 16 March 1993	Accession Number 69262
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: AD10-7-DH1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

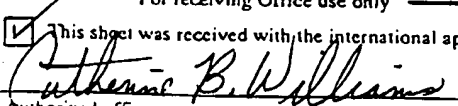
A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>12</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input checked="" type="checkbox"/></span>	
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Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69263
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
Escherichia coli: AD2-2-DH1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
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Date of deposit 16 March 1993	Accession Number 69264
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: G5d-1PstI-EcoRI-DH5	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>13</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69265
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: G2-2PstI-EcoRI-DH5	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
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*What Is Claimed Is:*

1. A method for detecting the presence of Neural Thread Protein (NTP) having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in a human subject, said method comprising:
  - (a) contacting a biological sample from said human subject that is suspected of containing said NTP with at least one molecule capable of binding to said protein; and
  - (b) detecting any of said molecule bound to said protein.
2. The method of claim 1, wherein said molecule is selected from the group consisting of:
  - (a) an antibody substantially free of natural impurities;
  - (b) a monoclonal antibody; and
  - (c) a fragment of (a) or (b).
3. The method of claim 1, wherein said biological sample is removed from said human subject prior to contacting said sample with said molecule.
4. The method of claim 1, wherein the detecting of any of said molecule bound to said protein is performed by *in situ* imaging.
5. The method of claim 1, wherein the detecting of any of said molecule bound to said protein is performed by *in vitro* imaging.
6. The method of claim 1, wherein said molecule is administered to said human subject.

7. The method of claim 1, wherein said molecule is bound to said protein *in vivo*.

8. A method of diagnosing the presence of Alzheimer's Disease in a human subject suspected of having Alzheimer's Disease which comprises:

5 (a) incubating a biological sample from said subject which is suspected of containing NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in the presence of at least one binding molecule capable of identifying said NTP; and

10 (b) detecting said binding molecule which is bound in said sample, wherein said detection indicates that said subject has Alzheimer's Disease.

9. The diagnostic method of claim 8, wherein said detection is by immunometric assay.

15 10. The diagnostic method of claim 9, wherein said immunometric assay is a monoclonal antibody-based immunometric assay.

11. The diagnostic method of claim 8, wherein said method comprises:

20 (a) incubating said biological sample with two different NTP monoclonal antibodies bound to a solid phase support; and

(b) detecting NTP bound to said monoclonal antibodies with a third different detectably labeled NTP monoclonal antibody in solution.

25 12. The diagnostic method of claim 8, wherein said incubating step further includes adding a known quantity of labeled Neural Thread Protein whereby a competitive immunoassay is established.

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13. The diagnostic method of claim 12, wherein said label is capable of emitting radiation.

14. The diagnostic method of claim 13, wherein said label is <sup>125</sup>I.

5 15. The diagnostic method of claim 8, wherein said detection is by immuno-polymerase chain reaction.

16. A method of diagnosing the presence of neuroectodermal tumors in a human subject suspected of having a neuroectodermal tumor which comprises:

10 (a) incubating a biological sample from said subject which is suspected of containing NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in the presence of at least one binding molecule capable of identifying said NTP; and

15 (b) detecting said binding molecule which is bound in said sample, wherein said detection indicates that said subject has a neuroectodermal tumor.

17. The diagnostic method of claim 16, wherein said detection is by an immunometric assay.

20 18. The diagnostic method of claim 17, wherein said immunometric assay is a monoclonal antibody-based immunometric assay.

19. The diagnostic method of claim 16, wherein said method comprises:

(a) incubating said biological sample with two different NTP monoclonal antibodies bound to a solid phase support; and

(b) detecting NTP bound to said monoclonal antibodies with a third different detectably labeled NTP monoclonal antibody in solution.

5       20. The diagnostic method of claim 16, wherein said incubating step further includes adding a known quantity of the corresponding labeled NTP whereby a competitive immunoassay is established.

21. The diagnostic method of claim 20, wherein said label is capable of emitting radiation.

22. The diagnostic method of claim 21, wherein said label is <sup>125</sup>I.

10       23. The diagnostic method of claim 16, wherein said detection is by immuno-polymerase chain reaction.

24. A method of diagnosing the presence of a malignant astrocytoma in a human subject suspected of having a malignant astrocytoma which comprises:

15       (a) incubating a biological sample from said subject which is suspected of containing NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in the presence of at least one binding molecule capable of identifying said NTP; and

20       (b) detecting said binding molecule which is bound in said sample, wherein said detection indicates that said subject has a malignant astrocytoma.

25. The diagnostic method of claim 24, wherein said detection is by an immunometric assay.

26. The diagnostic method of claim 25, wherein said immunometric assay is a monoclonal antibody-based immunometric assay.

27. The diagnostic method of claim 24, wherein said method comprises:

5 (a) incubating said biological sample with two different NTP monoclonal antibodies bound to a solid phase support; and

(b) detecting NTP bound to said monoclonal antibodies with a third different detectably labeled NTP monoclonal antibody in solution.

10 28. The diagnostic method of claim 24, wherein said incubating step further includes adding a known quantity of the corresponding labeled NTP whereby a competitive immunoassay is established.

29. The diagnostic method of claim 28, wherein said label is capable of emitting radiation.

30. The diagnostic method of claim 29, wherein said label is  $^{125}\text{I}$ .

15 31. The diagnostic method of claim 24, wherein said detection is by immuno-polymerase chain reaction.

32. A method of diagnosing the presence of a glioblastoma in a human subject suspected of having glioblastomas which comprises:

20 (a) incubating a biological sample from said subject suspected of containing NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in the presence of at least one binding molecule capable of identifying said NTP; and

25 (b) detecting said binding molecule which is bound in said sample, wherein said detection indicates that said subject suffers from a glioblastoma.

33. The diagnostic method of claim 32, wherein said detection is by an immunometric assay.

34. The diagnostic method of claim 33, wherein said immunometric assay is a monoclonal antibody-based immunometric assay.

5           35. The diagnostic method of claim 32, wherein said method comprises:

          (a) incubating said biological sample with two different NTP monoclonal antibodies bound to a solid phase support; and

          (b) detecting NTP bound to said monoclonal antibodies with  
10 a third different detectably labeled NTP monoclonal antibody in solution.

36. The diagnostic method of claim 32, wherein said incubating step further includes adding a known quantity of labeled NTP whereby a competitive immunoassay is established.

15           37. The diagnostic method of claim 36, wherein said label is capable of emitting radiation.

38. The diagnostic method of claim 37, wherein said label is  $^{125}\text{I}$ .

39. The diagnostic method of claim 32, wherein said detection is by immuno-polymerase chain reaction.

20           40. NTP substantially free of any natural impurities and having a molecular weight of about 42 kDa.

41. NTP substantially free of any natural impurities and having a molecular weight of about 26 kDa.

42. NTP substantially free of any natural impurities and having a molecular weight of about 21 kDa.

43. NTP substantially free of any natural impurities and having a molecular weight of about 17 kDa.

5 44. NTP substantially free of any natural impurities and having a molecular weight of about 14 kDa.

45. NTP substantially free of any natural impurities and having a molecular weight of about 8 kDa.

10 46. A recombinant DNA molecule comprising a genetic sequence coding for an NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa.

47. The DNA molecule of claim 46 wherein said NTP is human NTP.

48. The DNA molecule of claim 46 which is a plasmid.

15 49. A host transformed with the plasmid of claim 48.

50. A method of using the plasmid of claim 48 to prepare an NTP, said method comprising:

- (a) introducing said plasmid into a host cell to produce a recombinant host cell;
- (b) culturing said recombinant host cell; and
- (c) isolating said NTP from said recombinant host cell.



51. A DNA probe comprising a detectably labeled genetic sequence coding for an NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, or a fragment thereof.

5 52. A method of detecting the presence of a genetic sequence coding for NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in a clinical sample, which comprises:

- 10 (a) contacting said sample with the probe of claim 51 under conditions of hybridization; and
- (b) detecting the formation of a hybrid of said probe and said sequence.

15 53. A method of producing an NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, said method comprising:

- (a) culturing a recombinant host comprising a human gene coding for said NTP; and
- (b) isolating said NTP from said host.

20 54. The method of claim 53, wherein said gene is obtained from brain tissue of a patient with Alzheimer's Disease.

55. The method of claim 53, wherein said gene is obtained from a human neural tumor cell line.

56. The method of claim 53, wherein said gene codes for an NTP having a molecular weight of about 42 kDa.

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57. The method of claim 53, wherein said gene codes for an NTP having a molecular weight of about 26 kDa.

58. The method of claim 53, wherein said gene codes for an NTP having a molecular weight of about 21 kDa.

5 59. The method of claim 53, wherein said gene codes for an NTP having a molecular weight of about 17 kDa.

60. The method of claim 53, wherein said gene codes for an NTP having a molecular weight of about 14 kDa.

10 61. The method of claim 53, wherein said gene codes for an NTP having a molecular weight of about 8 kDa.

62. The method of claim 53, wherein said host is *E. coli*.

63. The method of claim 53, wherein said gene is contained by a vector.

15 64. The method of claim 53, wherein said gene is under control of an inducible promoter.

65. The method of claim 64, wherein said promoter is a lambda P<sub>L</sub> promoter.

66. The method of claim 64, wherein said promoter is a *tac* promoter.

20 67. A substantially pure NTP having a molecular weight of about 42 kDa obtained by the process of claim 53.

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68. A substantially pure NTP having a molecular weight of about 26 kDa obtained by the process of claim 53.

69. A substantially pure NTP having a molecular weight of about 21 kDa obtained by the process of claim 53.

5 70. A substantially pure NTP having a molecular weight of about 17 kDa obtained by the process of claim 53.

71. A substantially pure NTP having a molecular weight of about 14 kDa obtained by the process of claim 53.

10 72. A substantially pure NTP having a molecular weight of about 8 kDa obtained by the process of claim 53.

73. A 15- to 30-mer antisense oligonucleotide which is complementary to an NTP nucleic acid sequence and which is nonhomologous to the PTP nucleic acid sequence.

74. The antisense oligonucleotide of claim 73 which is DNA.

15 75. The antisense oligonucleotide of claim 73 which is an o-oligonucleotide.

76. The antisense oligonucleotide of claim 73 which is an S-oligonucleotide.

20 77. A pharmaceutical composition comprising at least one 15- to 30-mer antisense oligonucleotide which is complementary to an NTP sequence and which is nonhomologous to the PTP sequence; and a pharmaceutically acceptable carrier.

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78. A ribozyme comprising a target sequence which is complementary to an NTP sequence and nonhomologous to the PTP nucleic acid sequence.

79. A DNA molecule which codes for the ribozyme of claim 78.

5 80. A pharmaceutical composition comprising the NTP ribozyme of claim 78 and a pharmaceutically acceptable carrier.

81. A method for inhibiting the expression of an NTP in a patient, said method comprising administering to said patient an effective amount of the antisense oligonucleotide of claim 73.

10 82. A method for inhibiting the expression of an NTP in a patient, said method comprising administering to said patient an effective amount of the ribozyme of claim 78.

15 83. A method for inhibiting the expression of an NTP in a patient, said method comprising administering to said patient an effective amount of the DNA molecule of claim 79.

84. An oligonucleotide comprising the sequence 3'X5'-L-5'X3', wherein X comprises an NTP nucleic acid sequence which is nonhomologous to the PTP nucleic acid sequence, and wherein L represents an oligonucleotide linkage.

20 85. An oligonucleotide comprising the sequence 5'X3'-L-3'X5', wherein X comprises an NTP nucleic acid sequence which is nonhomologous to the PTP nucleic acid sequence, and wherein L represents an oligonucleotide linkage.

- 100 -

5 86. A method to treat diseases or conditions mediated by the presence of an NTP having a molecular weight of about 8 kDa, 14 kDa, 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, which method comprises administering to a patient in need of such treatment an effective amount of the oligonucleotide of claims 84 or 85, or a pharmaceutical composition thereof.

87. A ribonucleotide NTP External Guide Sequence comprising:  
10 (a) a 10-15 nucleotide sequence which is complementary to an NTP nucleic acid sequence and which is nonhomologous to the PTP nucleic acid sequence; and  
(b) a 3'-NCCA nucleotide sequence, wherein N is a purine.

88. The NTP External Guide Sequence of claim 87 which is DNA.

15 89. A method to treat diseases or conditions mediated by the presence of an NTP having a molecular weight of about 8 kDa, 14 kDa, 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, which method comprises administering to a patient in need of such treatment an effective amount of the ribonucleotide NTP External Guide Sequence of claim 87, or a pharmaceutical composition thereof.

90. An expression vector comprising the DNA molecule of claim 46.

20 91. A virion comprising the expression vector of claim 90.

92. A method to treat diseases or conditions mediated by the abnormally low level of expression of an NTP having a molecular weight of about 8 kDa, 14 kDa, 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, which method comprises administering to a patient in need of such treatment  
25 an effective amount of the virion of claim 91.

-101-

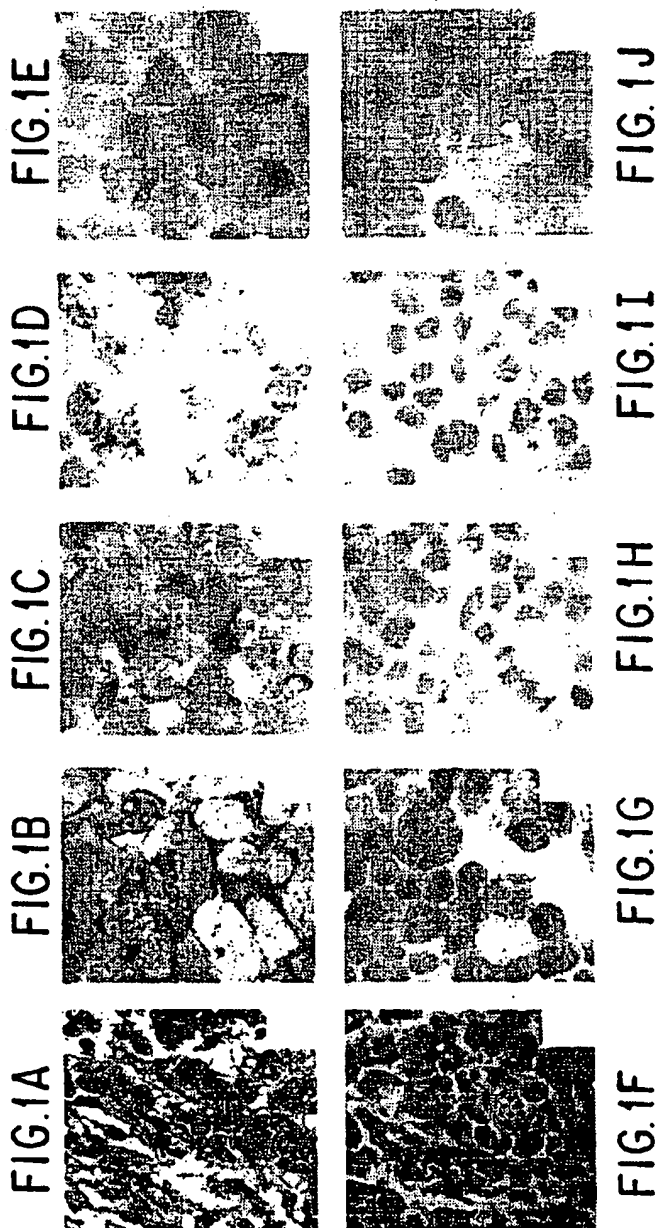
93. A method of differentiating between sporadic and familial Alzheimer's Disease in a human subject, said method comprising:

- (a) obtaining a biological sample from said human subject who is suspected of having Alzheimer's Disease;
- (b) purifying DNA from said biological sample; and
- (c) contacting said DNA with the probe of claim 51 under conditions of hybridization;

wherein familial Alzheimer's Disease is indicated by the detection of a hybrid of said probe and said DNA, and

wherein sporadic Alzheimer's Disease is indicated by the absence of detection of hybridization.

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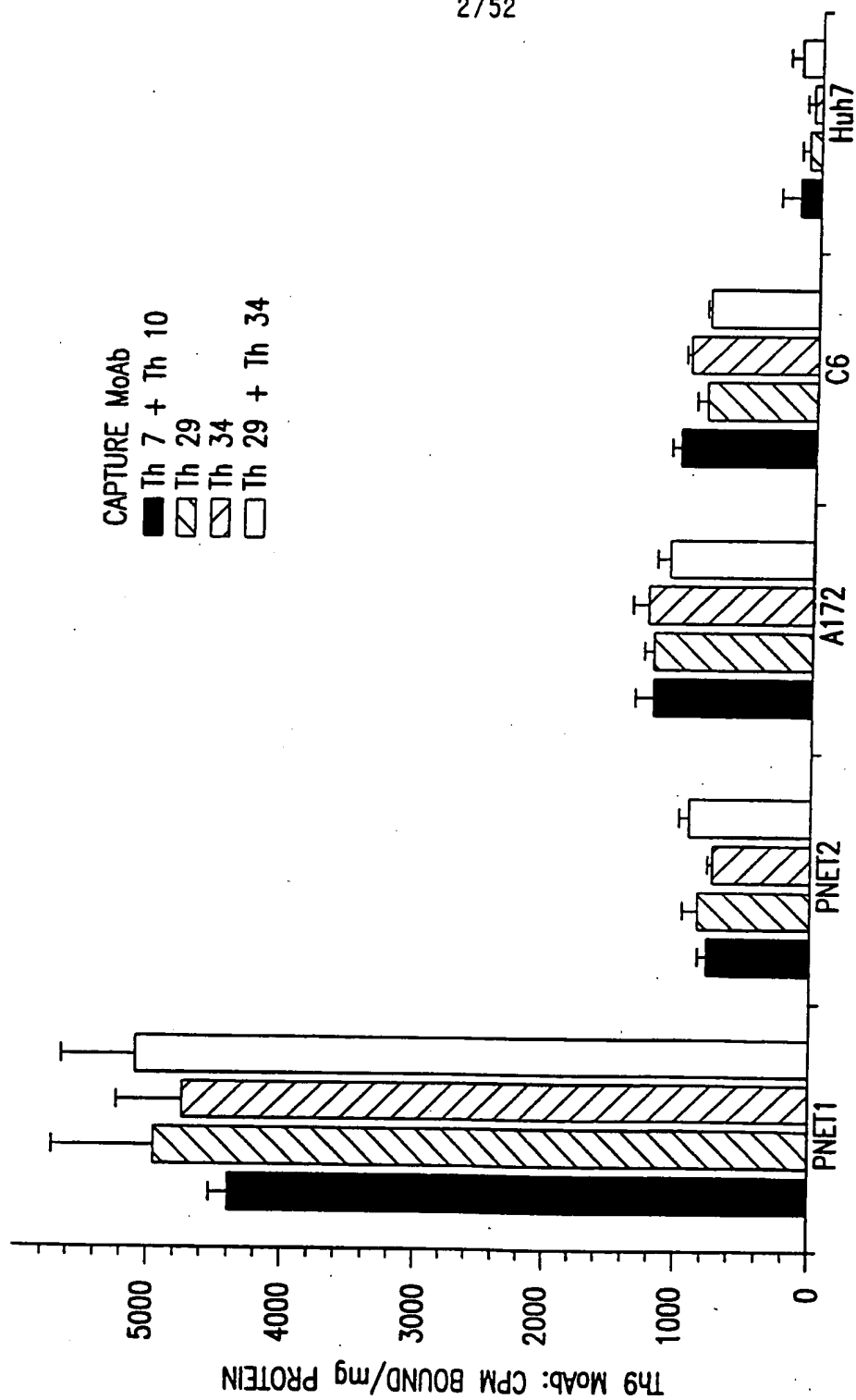


FIG.2



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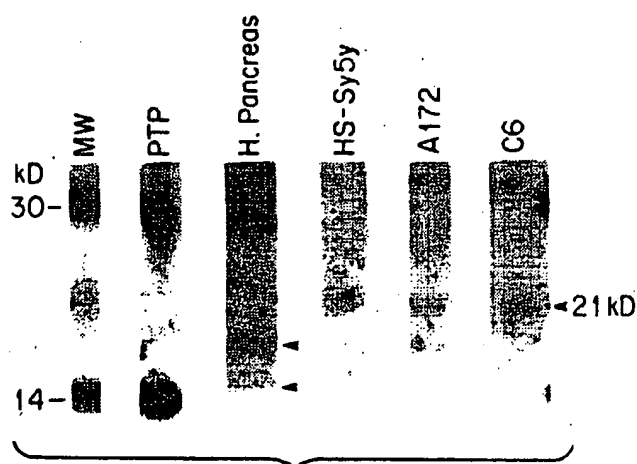


FIG. 3

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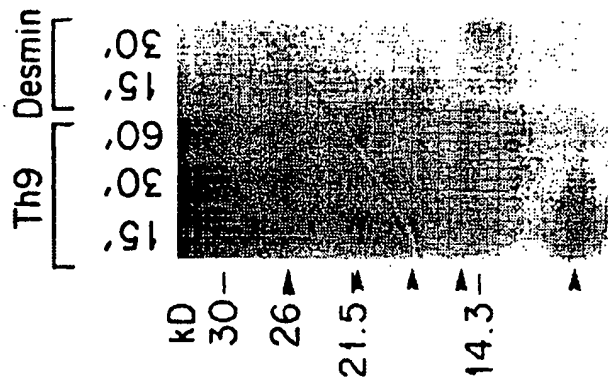


FIG.4B

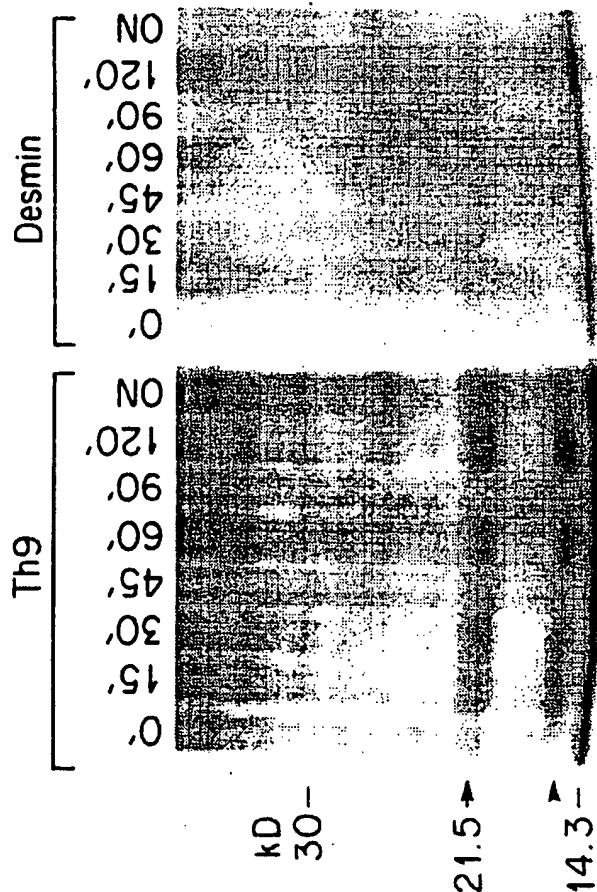


FIG.4A

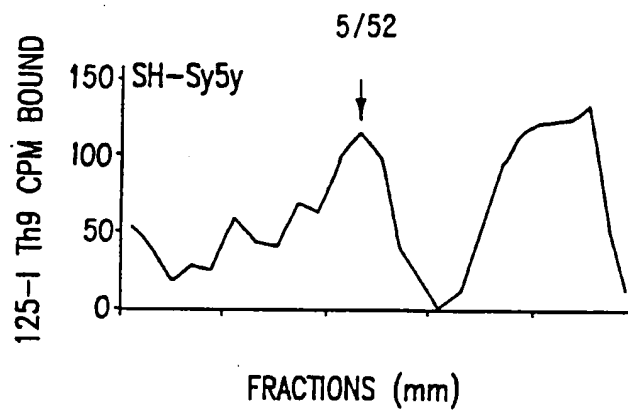


FIG.5A

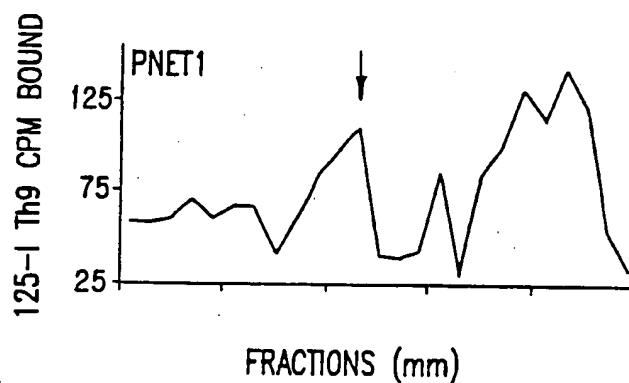


FIG.5B

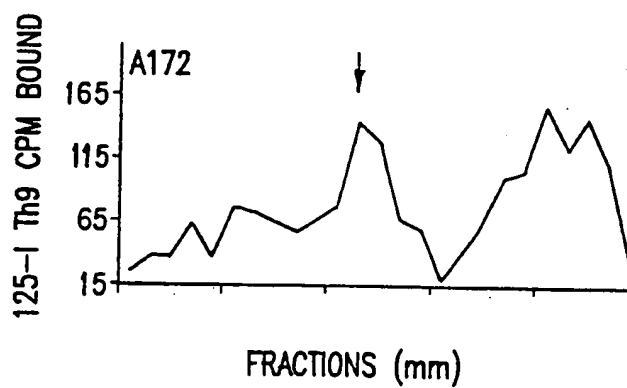


FIG.5C

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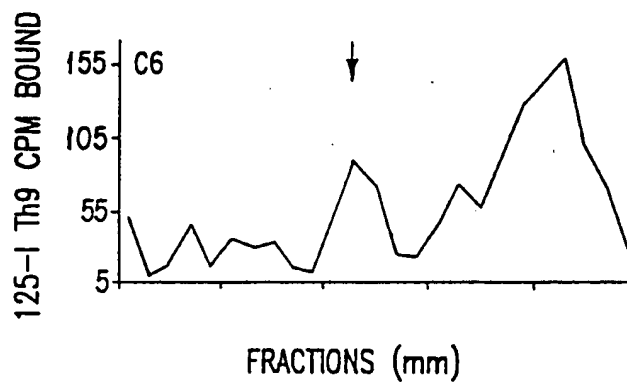


FIG.5D

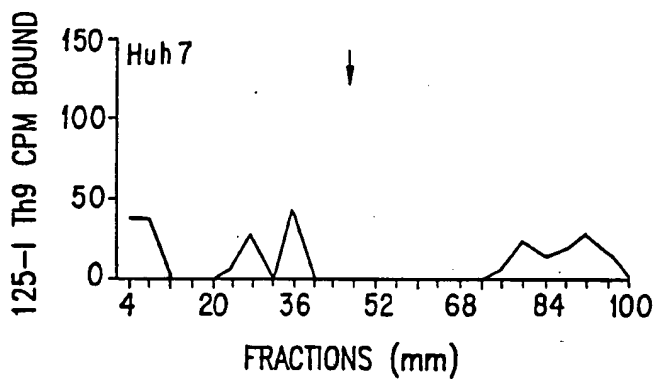


FIG.5E

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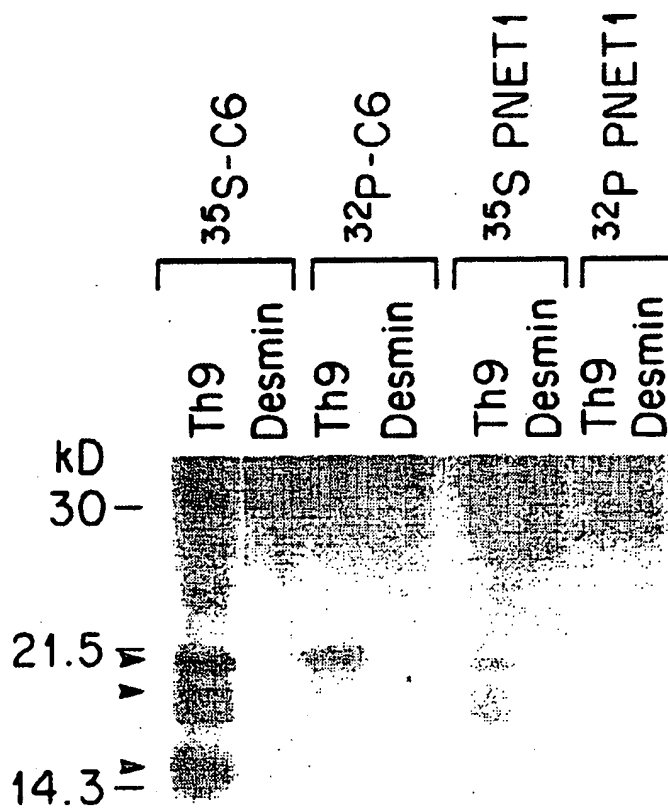


FIG. 6

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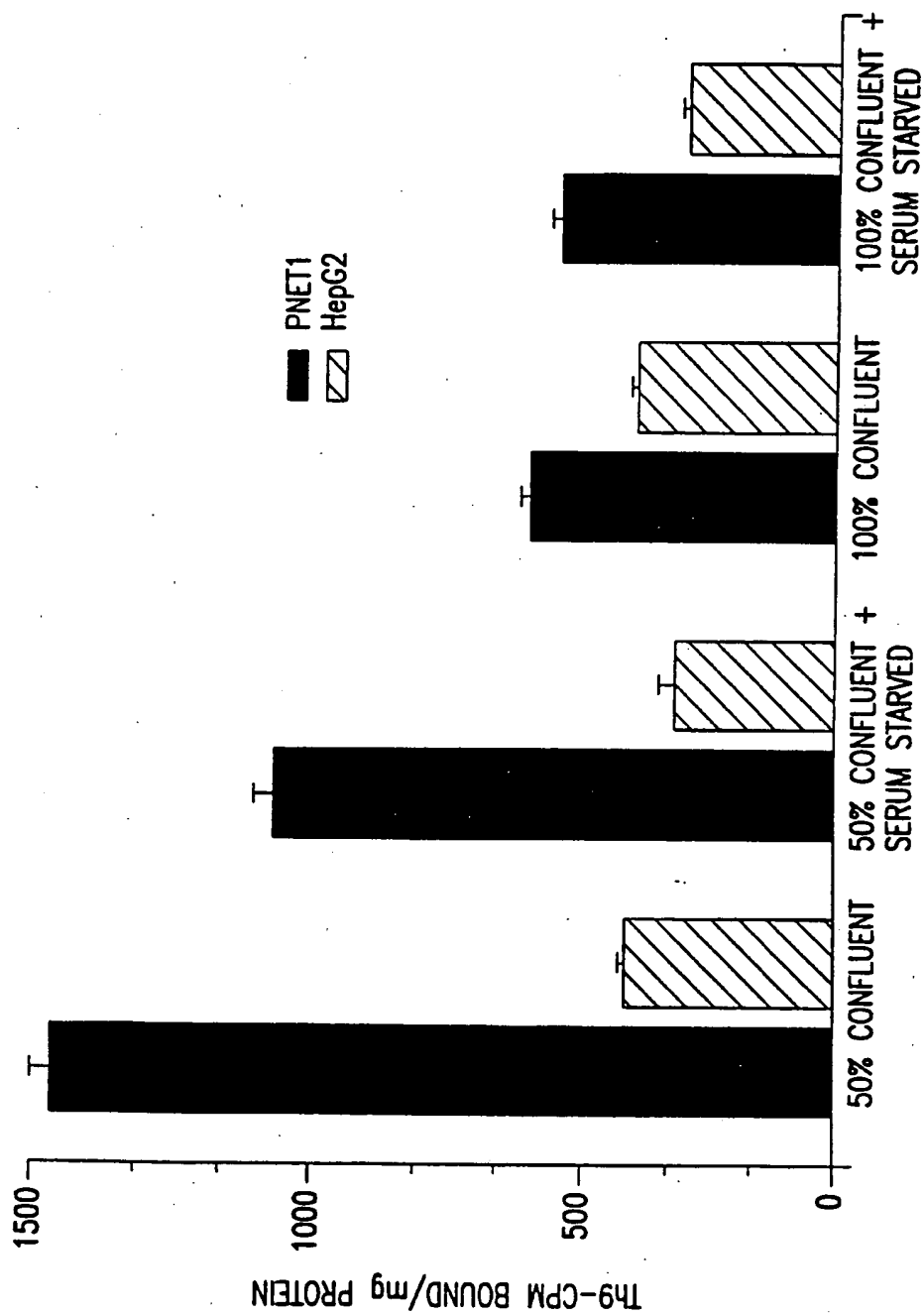


FIG. 7

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FIG. 8A



FIG. 8B



FIG. 8C



FIG. 8D



FIG. 8E



FIG. 8F

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## 1-9a T7 SEQUENCE

Sequence Range: 1 to 1442

```

CGCTG CGCCC AGGCT GGCTC TGGAA AGCCT GTGCG GTCCT GGCAG GAAGC CCGGC CCGTG   60
GAGCA GGTTC TCGTT CTGCT TCAGC AATAA ATAAG GGTGA CCACA GGGAC TTTGC TTTTG   120
GTTTC CTTTC CTGTG AAAAG GTTGG TTTTA AAGTG AGATA CACTT TTCCG TAGAA CAAGT   180
GTTCT ATCTT TAAAA ACCCA AATTG CAGCA CCGTG GATTA CTGGT CTCAG AACAA CTCAT   240
TGCGC ATCAG ATTG ACTCT CTGAT TTTCT GTCTA TTGGC CAAAT TGCCC TTAA CTGCA   300
CCTGA ATCCT TTGTG TACTG ATGCC TTTGA GCTGG GCACC TTGGG AGAGT GTTGT GTTGC   360
TGTTT ACGGT TCTTC CTTCC CTTG CTAAT TACAG TCTCT GGTGC CCAGC AAGCC CCTTT   420
GGCTT CCTTC CGTGA CTGGT CACGT TGTCT GCCTG GGCTC AGCGT GGACC TGCCC CATGC   480
TGCAG AACCT GGCCT CACCT GGACT TTTAC TAGAA TTGCC AGCTT CTCAA CTTAG CAGAT   540
CATCA CTCAT GCGGG CACAA GCAAA GATCA AACTT TTCTT TTTTG GTAAG CTTGA GTTTT   600
ACAAG TTATT TTTTG GTGAT GCGTA AGACA TTGCA GTGGG AAACC ATTCA ACTTG AGTTT   660
ATTGG AGTTT GCTGT TGTAG CAGGT TTTAA CTCAG GAACA ACTCT TGTCT GATCT CTCGC   720
CCCTC TGCCG GGACT ACATT ACTGT CTCTC GGAGC CCGTA GCGTT GCTGT CGAGT CCCAG   780
GACTA TCTCT GCAGA CTGCT ATGCT CAGAT CGAAG TATTT CACAA GAATA CTTGT GTTTT   840
TAACA GCCCT TCCCC TGGAC GGTGC GCCAT GAGGG CCTCA TGTTA CGCAT TGCCT TTTCT   900
TTCTG TGGAT CCAGT ATCTT CCTCG GCTTT TTAGG GAGCA GGAAA AATGC GTCTG AGACC   960
AACTC TTTT AAAA CCTGC CCTGT TGTAT ATAAC TGTGT CTGTT TCACC GTGTG ACCTC 1020
CAAGG GGGTG GGAAC TTGAT ATAAA CGTTT AAAGG GGCCA CGATT TGCCC GAGGG TTAAT 1080
CCTTT GCTCT CACCT TGTAT GGATG AGGAG ATGAA GCCAT TTCTT ATCCT GTAGA TGTGA 1140
AGCAC TTTCA GTTTT CAGCG ATGTT GGAAT GTAGC ATCAG AAGCT CGTTC CTTCA CACTC 1200
AGTCG CGTCT GTGCT TGTCC ACATG CGCTG GGCGT CTGGA CCTTG AATGC CTGCC CTGGT 1260
TGTGT GGACT CCTTA ATGCC AATCA TTTCT TCACT TCTCT GGACA CCCAG GGCGC CTGTT 1320
GACAA GTGTG GAGAA ACTCC TAATT TAAAT GTCAC AGACA ATGTC CTAGT GTTGA CTACT 1380
ACAAT GTTGA TGCTA CACTG TTGTA ATTAT TAAAC TGATT ATTTT TCTTA TGTA AAAAA 1440
AAA

```

FIG.9

## WP5' SEQUENCE

Sequence Range: 1 to 313

```

GATCC CGTTT GACAG GTGTA CCGCC CCACT CAAAC TCCCC ACCTG GCACT GTCCC CCGAG
CGGTC GCGCC CGCGC GACCA CCGAG CTCTG GGCGC CAGAA GCGAG AGCCC CTCGC TCCCC
CCCGC CTCAC CCGGT AGTGA AAAAA CGATG AGAGT AGTGG TATTT CACCG GCGGC CCGCG
AGGAC CCGCG CCGCA CCCAG TGCGG AACGG GGG

```

FIG.9A



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9A*1-T7									5	10	15	20
[ 386 ]									CAcc GlgGa TIA-C lgGlc>			
Human-PTP									CATT GCAGC TCAGC ATGCC			

9A*1-T7	25	30	35	40	45	50	55	60	65	70	75	
[ 386 ]	TCAGA	aCAoC	TCATt	gcgCA	T-CoG	ATlTo	CTeLc	TGAtt	TTTCT	GTCTo	llgGC	CAlIG>
Human-PTP	TCAGA	CCAGC	TCATA	CTTCA	TGCTG	ATCTC	CTGCC	TGATG	TTTCT	GTCTC	AGAGC	CAAGG

9A*1-T7	85	90	95	100	105	110	115		125	130	135	140
[ 386 ]	CCcIt	taaCl	gcocC	lGA-a	TcClI	lgIGl	aClGA	TCcIt	TGagC	IG-G	GCACC	-lTG->
Human-PTP	CCAAG	AGGCC	CAGAC	AGAGT	TGCCC	CAGGC	CCCGA	TCAGC	TGCCC	AGAAG	GCACC	AATGC

9A*1-T7	145	150	155	160	165	170	175	180	185	190	195	
[ 386 ]	ggAga	G-T-g	TlgTG	lTgCT	-gITT	AcgGl	lclLc	cT-tc	cCCTl	GcTaa	lTaCA	G-TCT>
Human-PTP	CTATC	GCTCC	TACTG	CTACT	ACTTT	AATGA	AGACC	GTGAG	ACCTG	GGTTG	ATGCA	GATCT

9A*1-T7	200	205	210	215	220	225	230	235	240	245	250	255
[ 386 ]	CTggT	CCCAG	cA-Ag	ccccT	llGCC	llCCT	lccGT	gacTG	gTCAC	gllGt	ClGcc	lGgGC>
Human-PTP	CTATT	GCCAG	AACAT	GAATT	CGGGC	AACCT	GGTGT	CTGTG	CT Q C	CCAGG	CCGAG	GGTGC

9A*1-T7	260	270	275	280	285	290	300	305	310	315		
[ 386 ]	CagcG	TGGCC	cCA-T	GcTgc	A-CAa	ccTGC	C-CTc	AgGAC	TTlLc	acT-a	GaATT	GcCCT>
Human-PTP	CTTTG	TGGCC	TCACT	GATTA	AGGAG	AGTGG	CACTG	ATGAC	TTCAA	TGTCT	GGATT	GGCCT

9A*1-T7	325	330	335	340	345	350	355	360	365	370	375	
[ 386 ]	lCcTc	A-aCl	lAgcA	GAlCa	llCaC	Tcatg	CgGGc	aCA-a	Gcaaa	gaTca	aCaCl	TlC-l>
Human-PTP	CCATG	ACCCC	AAAAA	GAACC	GCGGC	TGCA	CTGA	GCAGT	GGGTC	CCTGG	TCTCC	TACAA

9a-l7				10	15	20	25	30	35	40	45
[ 180 ]	TT lTCCT			AgA-A	cA-aG	-gGlt	cTatC	T-TTA	A-AA	-Accc	aaATT>
H REG GENE	TT CTCCT			ATAGA	GATTG	TTGAT	TTGCC	TCTTA	AGCAA	GAGAT	TCATT

9a-l7	50	55	65	70	75	80	85	90	95	100	105	110
[ 180 ]	GCAGC	aCcGC	lgGlc	TCAGA	aCAoC	TCATt	gcgCA	T-CoG	ATlTo	CTeLc	TGATt	TTTCT>
H REG GENE	GCAGC	TCAGC	ATGCC	TCAGA	CCAGC	TCATA	CTTCA	TGCTG	ATCTC	CTGCC	TGATG	TTTCT

9a-l7	115	120	125	130	135	140	145	150	155
[ 180 ]	GTCTo	lllGg	CcAaa	T-lGc	cCT-T	TTaaC	lgCac	ClgAo	TCTTT>
H REG GENE	GTCTC	AGAGC	CAAGG	TAAGA	TCTCT	TTTCC	ACCAA	CCAAC	TCTTT

FIG.10

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9A+1-T7  
[ 130 ]  
EXON2

	5	10	15	20	25	30
—————	CAC	cGlgG	aTIA-	CtgGt	CTCAG	AaCAa>
	CAT	TCCAG	CTCAG	CATGG	CTCAG	ACCAG

9A+1-T7  
[ 130 ]  
EXON2

	35	40	45	50	55	60	65	70	75	80
	CTCAT	tgcgC	AT-Co	GATIT	aCTct	CTGAT	ITTTT	TGTCT	allgG	CCAA>
	CTCAT	ACTTC	ATGCT	GATCT	CCTGC	CTGAT	GTTC	TGTCT	CAGAG	CCAA

H REG GENE  
[ 136 ]  
WPO3-4 T7

	5	10	15	20	25	30	35	40	45	
—————	G	aATtc	cTGgg	cTCAa	GtgAt	CCTC-	TCatG	caGTC	TCC-	CA-aA
	G	GAGIT	TTGTC	ATCAG	GCCAG	CCTCA	TCCCG	AGGTC	TCCTC	CACCA

H REG GENE  
[ 136 ]  
WPO3-4 T7

	50	55	60	65	70	75	80	85	95	100
	IG-gG	atgaC	AGGcT	-lGaG	C-CAC	C-AcA	-ccA	ggCCC	aT-Co	TCAGt
	CGTAG	CCAGC	AGGTT	CAGTG	CTCAC	CGAAA	GTAAA	ATCCC	CTCCT	TCAGC

H REG GENE  
[ 136 ]  
WPO3-4 T7

	105	110	115	120	125	130
	aAAaA	aAaAC	CTTAa	aaT-l	glTAg	GcAA- ATA>
	CAATA	TACAC	CTTAG	GTTCC	ACTAA	GTAAC ATA

WPO3 8SP  
[ 108 ]  
EXON2

	120	115	110	105	100	95	90	85	80	75
—————	<GTT-c	TgTGa	gTCTc	AAttt	gttcc	TTCTT	gGoAG	CT-G	tcTGG	-TgA-
	GTGTA	TTTGC	CTCTT	AAGCA	AGAGA	TTCAT	TGCAG	CTCAG	CATGG	CTCAG

WPO3 8SP  
[ 108 ]  
EXON2

	70	65	60	55	50	45	40	35	30
	<tTggI	cCcTC	lgLCT	GcToT	lCTGl	CTG-T	cTgTo	TGTCT	-G-t
	CTCAT	ACTTC	ATGCT	GATCT	CCTGC	CTGAT	GTTC	TGTCT	CAGAG

FIG.10A

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AD3-4-296		260	255	250	245	240	235	230	
[ 112 ]	-----	<ACTA	CcaAa	C-CT-	-GCat	tA-AA	-aAa	tltCg	gTtG- -GtCg
WP5' 4/93		ACCA	CGGAG	CTCTG	GGCGC	CAGAA	GGGAG	AGCCC	CTCGC TGCCC

AD3-4-296	225	220	215	210	205	200	195	190	185	180	175	170
[ 112 ]	<aCCtC	-ggAg	C-aGa	AcccA	Acctc	CGAgc	AGlac	A-TGc	TAaga	CltCa	cCoGl	CaaaG
WP5' 4/93	CCCGC	CTCAC	CGGGT	ACTGA	AAAAA	CGATG	AGAGT	AGTGG	TATTT	CACCG	GGCGC	CCCGC

AD3-4-296	165	160	155	150	145	140	135	130	125	120	115	
[ 112 ]	<-cGA-	aCgta	Ctota	CtCAa	T-lG	AtCco	otaAc	TtGaC	CoacG	Gaaco	AgTTA	ccCTA
WP5' 4/93	AGGAC	CCCCG	CCCGA	CCCAG	TGCGG	AACGG	GGGAG	TAGTC	CCGGG	GGCTC	ACTTA	TTCTA

AD3-4-296	105	100	95	90	85	80	75	70	65	60	55	50
[ 112 ]	<tAacA	G-CgC	Aatcc	tAttc	TAGAG	TCcAl	aTCAA	CAGGG	TtToC	gacCl	CGoTG	-Ttgg
WP5' 4/93	CATTA	GTCTC	ACGTG	CAGAC	TAGAG	TCAAG	CTCAA	CAGGG	TCTTC	TTTCC	CGCTG	ATTCC

AD3-4-296	45	40
[ 112 ]	<atCAg	GaC
WP5' 4/93	GCCAA	GTC

AD2 SP6F	10	15	20	25	30	35	40	45	50	55	60	65
[ 504 ]	AG-Tt	TCaCT	CTGTt	gCCCA	GGCTG	gAGTG	CAaTG	GCaCA	ATCct	GGCTC	ACTGC	aAcCT>
1-9AT7-3 3	AGATC	TGGCT	CTGTC	ACCCA	GGCTG	AAGTG	CAGTG	GCCCA	ATCTC	GGCTC	ACTGC	GAGCT

AD2 SP6F	70	75	80	85	90	95	100	105	110	115		
[ 504 ]	CCgCC	TCCCG	aGcTC	Aagca	ATTCT	CCTGC	CTCA-	-GCCT	C-G-	-TGA	GccGC	TGGGA>
1-9AT7-3 3	CCACC	TCCCG	GGTTC	ACTTC	ATTCT	CCTGC	CTCAC	TGCCT	CAGCC	TCTGA	GTAGC	TGGGA

FIG.10B

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## HB4-SEQ SEQUENCE

```
GAGGC GTATT ATACC ATGCT CCATC TGCCT ACGAC AAACA GACCT AAAAT CGCTC ATTGC 60
ATACT CTTCA ATCAG CCACA TAGCC CTCGT AGTAA CAGCC ATTCT CATCC AAACC CCCTG 120
AAGCT TCACC GGCGC AGTCA TTCTC ATAAT CGCCC ACGGG CTTAC ATCCT CATT A CTATT 180
CTGCC TAGCA AACTC AACTC ACGAA CGCAC TCACA GTGGC ATCAT AATCC TCTCT CAAGG 240
ACTTC AACTC CTA CTACT CCCAC TAATA GCTTT TTGAT GACTT CTAGC AAGCC TCGCT AACCT 300
CGCCT TACCC CCCAC TATTA ACCTA CTGGG AGAAC TCTCT GTGCT AGTAA CCACG TTCTC 360
CTGAT CAAAT ATCAC TCTCC TACTT ACAGG ACTCA ACATA CTAGT CACAG CCCTA TACTC 420
CCTCT ACATA TTTAC CACAA CACAA TGGGG CTCAC TCACC CACCA CATT A ACAAC ATAAA 480
ACCCCT CATT C ACACG AGAAA ACACC CTCAT GTTCA TACAC CTATC CCCCC TTCTC CTCCT 540
ATCCC TCAAC CCCGA CATCA TTACC GGGTT TTCCT CTAA AAAAA AAAAA AAAA 590
```

## HB4 PROTEIN

```
EAYYT MLHLP TTNRP KIAHC ILFNQ PHSPP SNSHS HPNPL KLHRR SHSHN RPRAY ILITI 60
LPSKL KLRTH SQSHH NPLSR TSNST PTNSF LMTSS KPR 95
```

FIG.11A

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HB4 PROTEIN HYDROPHILICITY WINDOW PLOT

HYDROPHILICITY WINDOW SIZE = 7      SCALE = Kyle-Doolittle

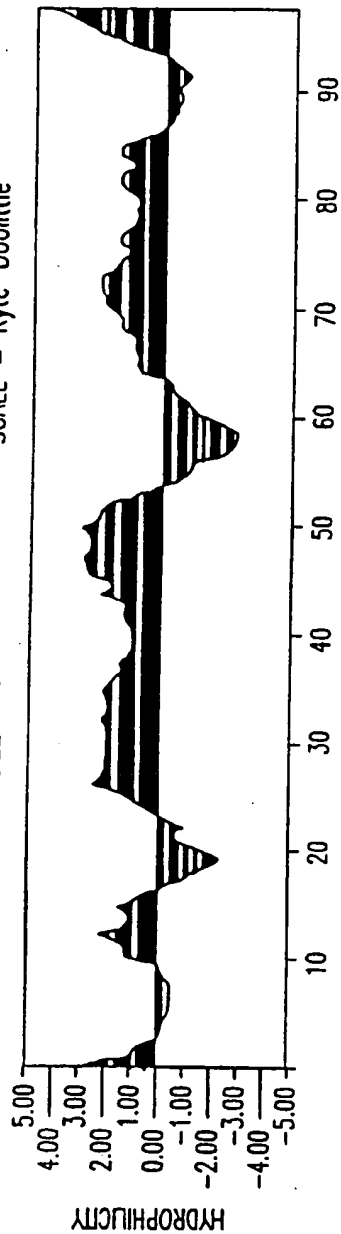


FIG.11B

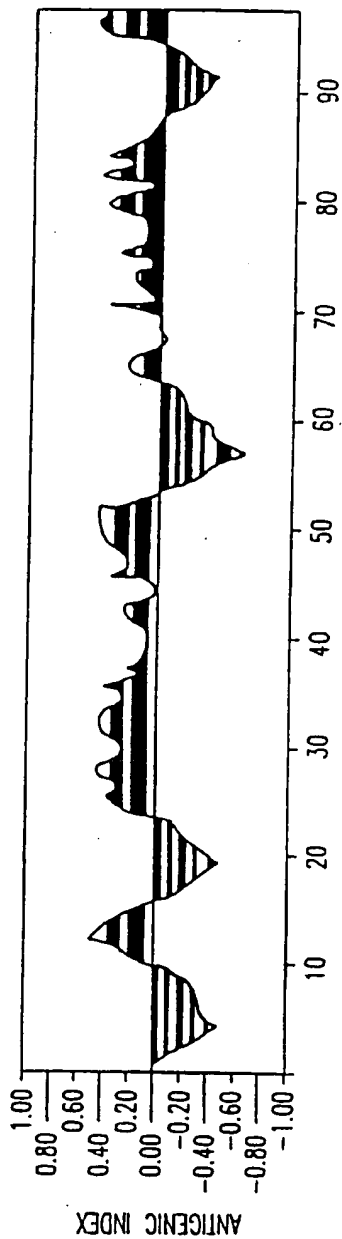


FIG.11C

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HB4 SEQ

[ 440 ]

Human-PTP

-AToC&gt;

ATGC

HB4-SEQ 15 20 25 30 35 40 45 50 55 60 65  
 [ 440 ] C-AT- GCTCC aLCTG C-CT ACgac AA-ac AGACC -T-A- AaaTc GcTco lTGCA lA-CT>  
 Human-PTP CTATC GCTCC TACTG CTA CT ACTT AATGA AGACC GTGAG ACCTG GGTG ATGCA GATCT

HB4-SEQ 70 75 80 85 90 95 100 105 110 115 120  
 [ 440 ] CTlco aLcAG cACAT -Agcc ClcG- lAgla ocaG- CcaTl CTCAl CCAaa CCccc tGaag>  
 Human-PTP CTATT GCCAG AACAT GAATT CGGGC AACCT GGTGT CTGTG CTCAC CCAGG CCGAG GGTGC

HB4-SEQ 125 130 135 140 145 150 155 160 165 170 175  
 [ 440 ] CTTco ccGgC gCagT cATT- clcAt AoTcG C-Cco cgGgC TTacA T-cCT -cATT acLoT>  
 Human-PTP CTTTG TGGCC TCACT GATTA AGGAG AGTGG CACTG ATGAC TTCAA TGTCT GGATT GGCCT

HB4-SEQ 180 185 190 195 200 205 210 215 220 225 230 235  
 [ 440 ] lC-TG cCaqC AAAct cAAoC laCGa acGCA CT-ca -CAGT cGcat CaTaa TCTCl clCAA>  
 Human-PTP CCATG ACCCC AAAAA GAACC GCCGC TGGCA CTGGA GCAGT GGGTC CCTGG TCTCC TACAA

HB4-SEQ 240 245 250 255 265 270 275 280 285 290 295 300 305  
 [ 440 ] GgoCT -lcaa AcTcl AcLCC CAAGC lTGT gAcTl CTaGC aACcl cGctA aCCtc gCCTt>  
 Human-PTP GTCCT GGGGC ATTGG AGCCC CAAGC AGTGT TAATC CTGGC TACTG TGTGA GCCTG ACCTC

HB4-SEQ 310 315 320 325 330 340 345 350 355 360 365 370  
 [ 440 ] AccCc CActA TTaac clAct GGgAG aATGT G-CTa GT-AA -cCAc GTTCT CCTTc aaoTa>  
 Human-PTP AAGCA CAGGA TTCCA GAAAT GGAAG GATGT GCCTT GTGAA GACAA GTTCT ccTTT GTCTG

HB4-SEQ 375 380 385 390 395 400 405 410 415 420 425  
 [ 440 ] lCAct clccl AcLTA cAGG- A-CT- cAAcA TAcLa GTCcA GccCT -AToC lcCcl cTACA>  
 Human-PTP CAAGT TCAAA AACTA GAGGC AGCTG GAAAA TACAT GTCTA GAACT GATCC AGCAA TTACA

HB4-SEQ 430 435 440 445 450 455 460 465 470 475 480 485  
 [ 440 ] lalll acCAc AAcac AAlgg GGclC A-CTC aCCcA C-CAc aTlAA CCato AoAcC CTCaT>  
 Human-PTP ACGGA GTCAA AAATT AAACC GGACC ATCTC TCCAA CTCAA CTCAA CCTGG ACACT CTCTT

HB4-SEQ 490 495 500 505 510 515 520 525 530 540 545  
 [ 440 ] -TCac acGAG -aaaa Ccccc TcATg TTC-A TAcac cTA- TcCCC CAITC TTccl ATCCc>  
 Human-PTP CTCTG CTGAG TTTGC CTTGT TAATC TTCAA TAGTT TTACC TACCC CAGTC TTTGG AACCT

HB4-SEQ 550 555 560 565 570 575 580 585 590  
 [ 440 ] TcAAc cccgA cAlcA AcCgg GTTTC ClCTl AAAAA AAAAA AAAAA A>  
 Human-PTP TAAAT AATAA AAATA AACAT GTTTC CACTA AAAAA AAAAA AAAAA A

FIG.11D

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H REG GENE 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305  
 [ 284 ] —C tTcTT -TttC AgGC- CoAgo gGCCc A-GAC AgAgl tgCC- ccAgg CcCgg ATcag>  
 HB4-SEQ C GTATT ATACC ATGCT CCATC TGCCT ACGAC AAACA GACCT AAAAT CGCTC ATTGC

H REG GEN2310 2315 2320 2322330 2335 2340 2345 2350 2355 2360 2365 2370  
 [ 284 ] cTgCc CagaA ggCAc CoACc TAtCg CTCcT AcT-g CtaCt AcTtT aATga AgACC gCgaG>  
 HB4-SEQ ATACT CTTCa ATCAG CCACA TAGCC CTCGT AGTAA CAGCC ATTCT CATCC AAACC CCCTG

H REG GBNE 2375 2380 23852390 2395 2400 2405 2410 2415 2420 2425 2430  
 [ 284 ] -AcCT gggll GatGC AGTgt gagTg AggAg aGCgt gtGGG aaggg AgaCT CATga -aggg>  
 HB4-SEQ AAGCT T QCC GGCGC AGTCA TTCTC ATAAT CGCCC ACGGG CTTAC ATCCT CATTa CTATT

H REG GENE 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485  
 [ 284 ] agGgg aAGC- lgC-C AcLCT -CcAg tGlgl TCAgt GgCGC Aatga gAT-g agaCT gAAcc>  
 HB4-SEQ CTGCC TAGCA AACTC AAACt ACGAA CGCAC TCACA GTCCG ATCAT AATCC TCTCT CAAGC

H REG GENE 24902495 2500 2505 2510 2515 2520 2525 2530 2535 2540  
 [ 284 ] cCTTt AIACT aTcaT CagcC cCA-A aCTTT ccaAT -CTa CT-l lAlCC -ColT AllCa>  
 HB4-SEQ ACTTC AAACt CTACT CCCAC TAATA GCTTT TTGAT GACTT CTAGC AAGCC TCGCT AACCT

H REG GENE2545 2550 2555 2560 2565 2570 2580 2585 2590 2595 2600  
 [ 284 ] gcaCa TlCCC agCAC aAagA ACCTg gTGGG lG-AC agcaT catC- AcggA Catta cTCTg>  
 HB4-SEQ CGCCT TACCC CCCAC TATTA ACCTa CTGGG AGAAC TCTCT GTGCT AGTAA CCACG TTCTC

H REG GEN2605 2610 2612620 2625 2630 2635 2640 2645 2650 2655 2665 2670  
 [ 284 ] CTG-T CcLtt LTCAC cCTCC T-CTT ggAGG ACTCA glATA tccGT CACAa CCCTc cACTg>  
 HB4-SEQ CTGAT CAAAT ATCAC TCTCC TACTT ACAGG ACTCA ACATA CTAGT CACAG CCCTa TACTC

H REG GENE 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720  
 [ 284 ] ogTCT cCAT- TTT-C lTc- lgCAA co-G CTCta T-tgC CAgaA CATga A-ttC gggcA>  
 HB4-SEQ CCTCT ACATA TTTAC CACAa CACAa TGGGG CTCAC TCACC CACCA CATTa ACAAC ATAAA

H REG GENE 2725 2730 2735 2740  
 [ 284 ] A-CCT -ggTg tC-lG lG-c lCACC C>  
 HB4-SEQ ACCCT CATTc ACACG AGAAA ACACC C

FIG.11E

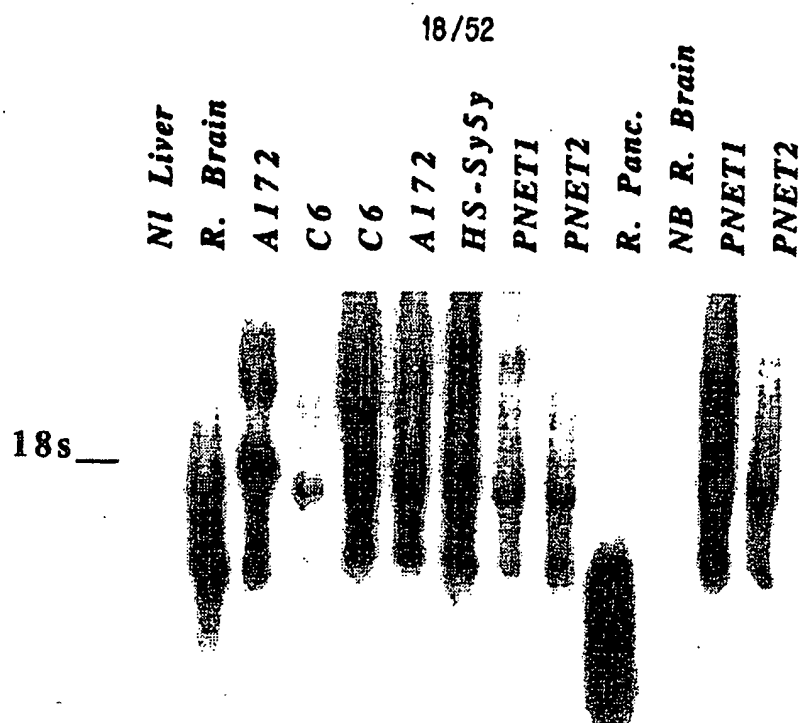


FIG.12A

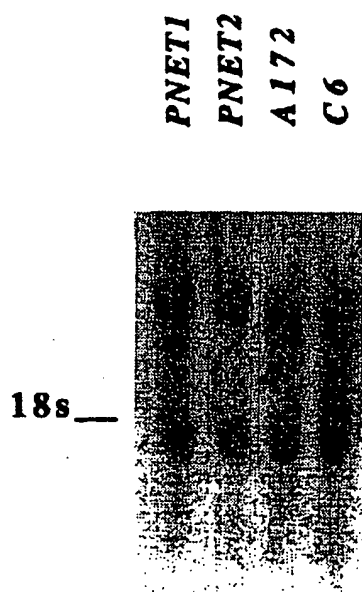


FIG.12B

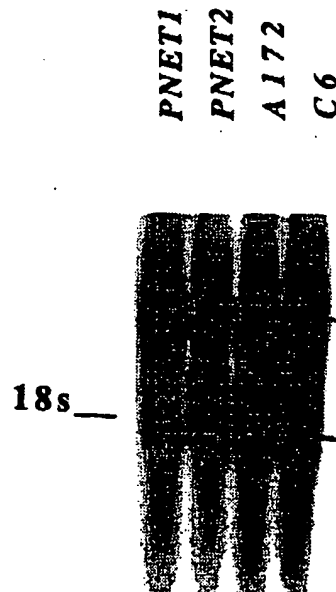


FIG.12C



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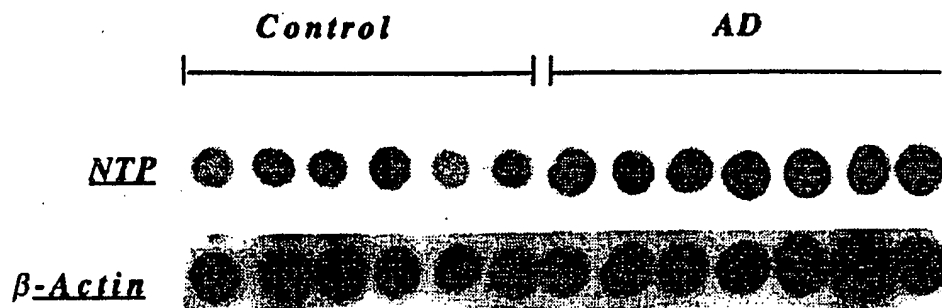


FIG. 13A

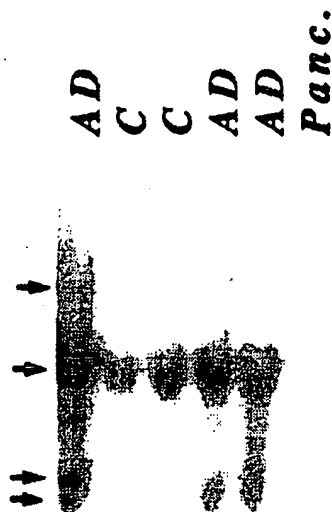


FIG. 13B

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PNET1  
PNET2  
SH-SY5Y  
A172  
C6  
C6  
NB Brain  
AD  
CONTROL



1-9a

FIG.14A



FIG.14B

1-9a



O-18

FIG.14C

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SE-RT / PCR CLONES

SE (1) SE (2) SE (3) SE (4) SE (5) SE (6) SE (7)



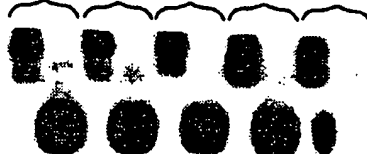
1-9a

FIG. 15A

SW 151

018-3-1 UPPER PROBE  
O/N EXPOSURE 1-27-93

SE (3) SE (4) SE (5) SE (6) SE (7)



0-18

FIG. 15B

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AD2-2 T7

```

GTTCT TAGTC TATCT CTTGT ACAA CGATG TGCTT TGAAG ATGTT AGTGT ATAAC AATTG 60
ATGTT TGTTC TCTGT TTGAT TTAA ACAGA GAAAA AATAA AAGGC GTAA TAGCT CCTTT 120
TTTCT TCTTT CTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 180
ACAGA GGGAT ATGCT GTAGA GTGTT TTTAT TGCCT AGTTC ACAA GCTGC TTTG AATGC 240
TGGTG GTTCT ATTCC TTTGC ACATC ACGAC ATTTT ATAAT CATAG TTAA TCGTA TATGA 300
CAAAA ATGCT CTGAT CTGAT GCCAA AGGTC AATTC AGTGT ATATA ACCTG AACAC ACTCA 360
TCCAT TCGT TT 372

```

AD2-2 T7 PEP

```

MFVFC LILNR EKIKG GNSSF FLLSF FFSFQ NCCQC FCRT TEGYA VECFY CLVDK AAFEC 60
WVFYS FDT

```

FIG.16A

AD2 SP6F

```

ACTGT CTCCC CCTTT GATAG GGACA CTAA GTGGT CTGTA CTTGG GTAGA GGATG GCANG 60
TTAAG AATTA AAATC GTCTG GGTGC GGTCT GCAAG CTTGT AATCC CAGCA CTTG GGAGG 120
CTGAG GCGGG GGGAT CACCT GAGGT CAGGA GTTCG ACACC AGCCT GATGA ACATG GAGAA 180
ACCCC ATCTC TACTA AAAAT ACAA TATTA GCTGG GCGTT GTCCG GCGCC TGTA TCCCA 240
GCGGC TCACG AGGCT GAGGC AGGAG AATTC CTGTA GCTCG GGATG GCGGA GGTTC CAGTG 300
AGCCA GGATT GTGCC ATTGC ACTCC AGCCT GGGCA ACAAG AGTGA AACTC TGTCT CAAAA 360
AAAAA AAAAA AAAAA AA 377

```

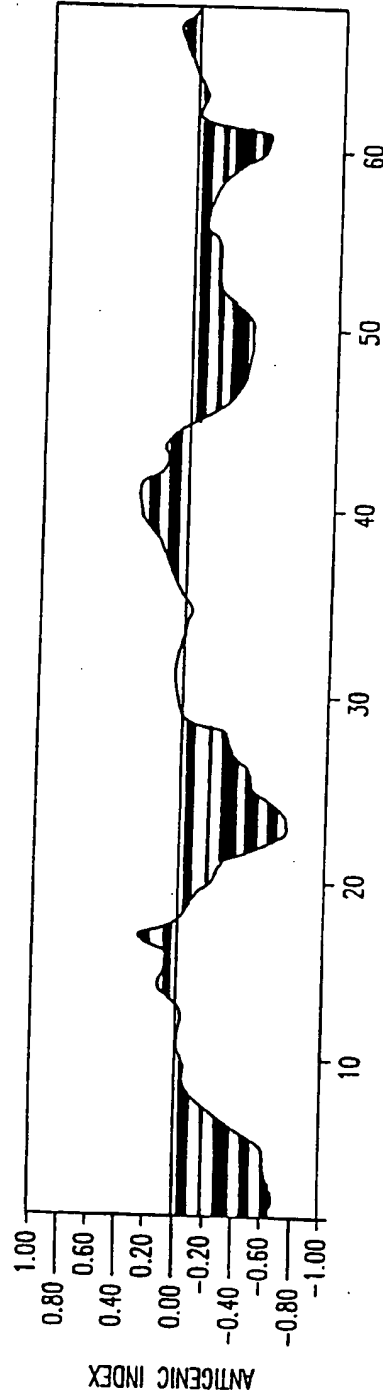
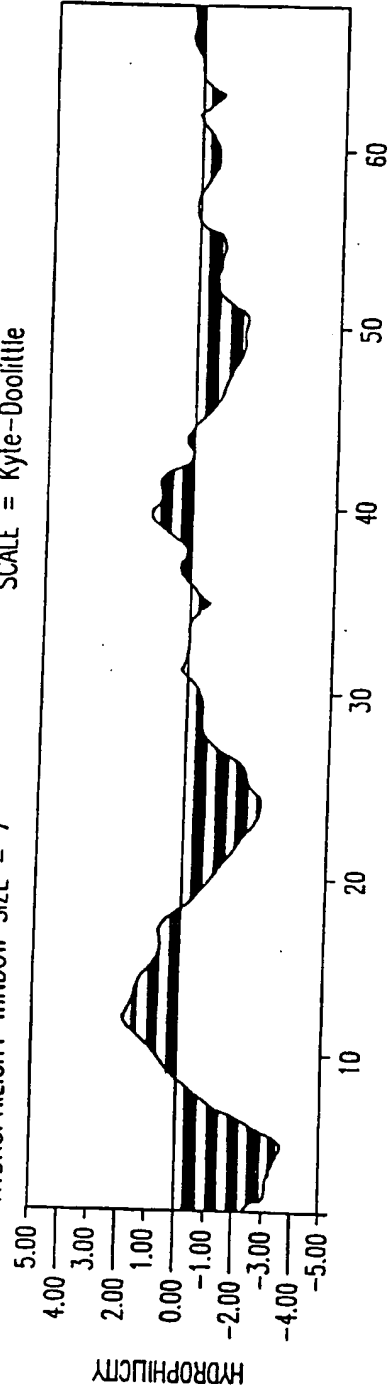
FIG.16D

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AD2-2 T7 HYDROPHILICITY WINDOW PLOT

HYDROPHILICITY WINDOW SIZE = 7

SCALE = Kyte-Doolittle



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## AD2-2 SEQUENCE

```
GGGTAAACAC ATTTTGTTC TTAGTCTATC TCTGTACAA ACGATGTGCT TTGAAGATGT 60
TAGTGATATA CAATTGATGT TTGTTTCTG TTTGATTTA AACACAGAAA AAATAAAAGG 120
GGGTAATAGC TCCTTTTTC TTCTTTCTT GATTTTAAAC AGAGAAAAAA TAAAAGGGGG 180
TAATAGCTCC TTTTTCCTC TTCTTTTTC TTTTTCATT TCAAATTGC TGCCAGTGTT 240
TTCAATGATG GACAACAGAG GGATATGCTG TAGAGTGTG TATGCTAG TTGACAAAGC 300
TGCTTTGAAT GCTGGTGGT CTATTCCTT GACACTAGC ACTTTTATA TACATGTAA 360
TGCTATAGGA CAAGATGCTC TGATTCCTG GTGCCAGAG TTCAATTCAG TGTATATAAC 420
TGAACACACT CATCCATTG TGCTTTTGT TTTTATGG TGGCTTAAAG GTAAAGAGCC 480
CATCTTTGC AAGTCATCCA TGTGTTACT TAGGCATTT ATCTTGGTC AAATTGTTGG 540
AAGAATGGT GCTTGTTC TGTGTTTGT ATTTGTGCT AATGCACGT TTAACATGAT 600
AGACCAATC CATGTGTAG CTAGTTTCT GGAAAAGTCA ACTCTTTAG GAATTGTTT 660
TCAGATCTC AATAAATTT TTCTTTAAAT TTCAAAGAAC AATGTGCTG TGTGATGCC 720
TTACAAAAAC CATTGTATAT TTGTGATTC CTCTTGAT TTACAGAGT GTTTTCAGG 780
TGGTGCTTT GTTTCTGGT ATGGCCTTA TGAATGAGA CGCTTAGCT TTGGTACGT 840
GGGTAATCC ATAGCAGCTT TGGCAGTTC GTCTCTGAG TCTAGCTAA AAAGTAGAA 900
GTTTACATG CTGTTTTTT TATTTCCCT AAATTATTAC TTAGCTGAG CATTAAATTA 960
GGGCATTTT ACCTGTGTAA AATTATGTC AGCTTTTTT TGTCTATAAT TGTTTACTTT 1020
TGTGGTTTA CTCTAGAAAC ATGAGCCAAA AATGTCAATA GACAACACAG TATTAATAA 1080
ACCCAAAAGT GTAAAGGGC AACGTTTCT CCTTTGATA GGGACACTAA AGTGGTCTGT 1140
ACTTGGGTAG AGGATGGCAG ACGTTAAGAA TTAATGCG TCTGGTGGC GTCTCAGCT 1200
TGTAATCCCA GCACTTTGGG AGGCTGAGC GGGCGGATCA CCTGAGTCA GGAGTTGAC 1260
ACCAGCTGA TGAACATGA GAAACCCAT CTCTACTAA AATACAAATA TTAGCTGGC 1320
GTTGTGGC GCCTGTAAT CCAGCGGCT ACGAGGCTG GGCAGGAGAA TTGCTTGAGC 1380
TCGGATGGC GGAGTTGCA GTGAGCCAG ATTGTCCAT TGACTCCAG CCTGGCAAC 1440
AAGAGTGAAC CTCTGTCTA AAAAAAAAA AAAAAAAAA 1480
```

FIG.16E

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## AD3-4 SEQUENCE

ATGAT GGTCT GTTGG AATCG GTTTG GTAAA TGGGT TTATT TCATA TCCGC TATCT TTAAC 60  
 TTTGG ACCGC GTTAT CTATA TCATG GCGTT CCTTT CTA CT TTTA ATATT GGTTC GTATT 120  
 ATATC GTTCC TGATT GGGGA TATGG AAGAC GTATT ACTTA ATTGT ACTTT ATTGA AACGT 180  
 TCCTC TCGGT TTCGA TTCTG GGGGC TTTGG TCTGC TCGAT GGATT CTGTG CGATT TTCTC 240  
 GTGTG GCAGT AACAT ACCGT TTTAT CACCC TTCTA AATAT CCCAT CTCCC GCTGT TTGGT 300  
 AGGCT CGGAA CACTA TCGAC CAACA GGTTC TATCT AGAAT CAACT TCGAA ATTAA ACGGT 360  
 GTCTT GG 367

## AD3-4 PROTEIN

MMVCW NREGK WYFII SAIFN FGPRY LYHGV PFYFL ILVRI ISFLI GDMED VLLNC TLLKR 60  
 SSRFR FWGAL VCSMD SCRF S RVAVT YRFIT LLNIP SPAVW MARNT IDQOV LSRIK LEIKR 120  
 CL 122

FIG.16F

## AD3-4T7

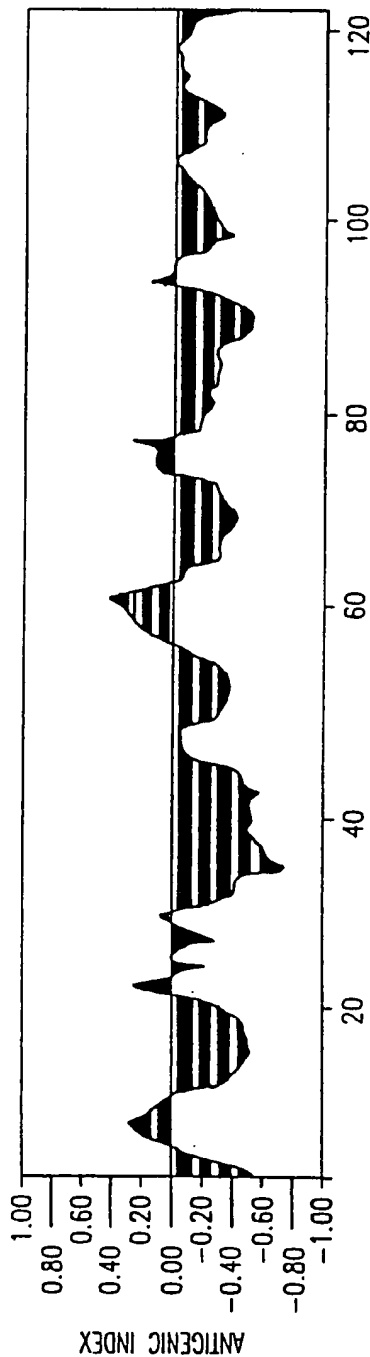
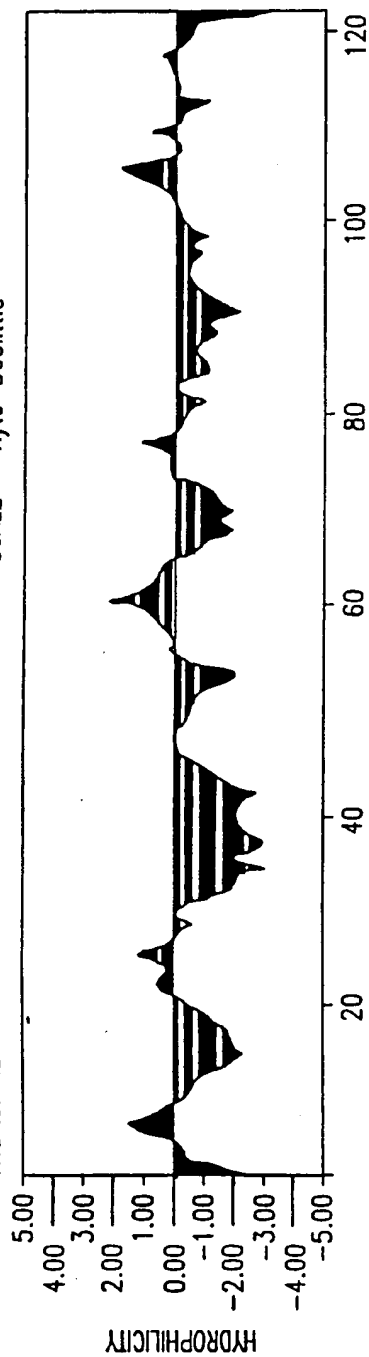
CCCAC AGGTC CTAAG CTACC AAACC TGCAT TAAAA AATTT CCGTT GGTGG ACCTC GGAGC 1180  
 AGAAC CCAAC CTCCG AGCAG TACAT GCTAA GACTT CACCA GTCAA AGCGA ACGTA CTATA 1240  
 CTCAA TTGAT CCAAT AACTT GACCA ACGGA ACAAG TTACC CTAGG GATAA CAGCG CAATC 1300  
 CTATT CTAGA GTCCA TATCA ACAAT AGGGT TTACC ACCTC GATGT TGGAT CAGGA CATCC 1360  
 CGATG GTGCA GCGGC TATTA AAGGT TCGTT TGTTC AAACG ATTAA AGTCC TCGTG TCTGA 1420  
 GTTCA GACCG AAGTA ATCCA GGTGG GTTTC TATCT TCTTC AAATT CCTCC CTGTA CCGAA 1480  
 AGGAC TAATG AGAAA TAAGG CCTAC TTCAC AAAGC GGCCT TCCCC CGTAA TGATA TCATC 1540  
 TCAAC TTAGT ATTAT ACCCA CACCC ACCCA AGAAC AGGGT TTGTT AAAAA AAAAA AAAAA 1600

FIG.16I

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AD3-4 HYDROPHILICITY WINDOW PLOT

HYDROPHILICITY WINDOW SIZE = 7      SCALE = Kyle-Doolittle





## AD3-4SP SEQUENCE

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AACCCACTCC ACCTTACTAC CAGACAACCT TAGCCAAACC ATTTACCCAA ATAAAGTATA 60  
 GCGGATAGAA ATTGAAACCT GCGCAATAG ATATAGTACC GCAAGGAAAG ATGAAAAAT 120  
 ATAACCAAGC ATAATATAGC AAGGACTAAC CCCTATACCT TCTGCATAAT GAATTAACAT 180  
 GAAATAACTT TCCAAGGAGA GCCAAAGCTA AGACCCCGA AACCAGACGA CCTACCTAAG 240  
 AACAGCTAAA AGAGCACACC GTCATTGTAT GGCAAAATAG TGGGAAGATT TATAGGGTAG 300  
 AGGGCGACAA ACCATCCGAG CCTTGTGATA GCTGGTGTG CAAGATAGAT CTTAGTTCAA 360  
 CCTTTAATTT GCCACAGAAC C 381

FIG.16J

## AD3-4T7 SEQUENCE

TTTTTTTTTT TTTTAAACAA ACCCTGTTCT TGGGTGGGTG TGGGTATAAT ACTAAGTTGA 60  
 GATGATATCA TTACGGGGGA AGGCGCTTT GTGAAGTAGG CCTTATTTCT CATTAGTCCT 120  
 TTCGGTACAG GGAGGAATTT GAAGAAGATA GAAACCGACC TGGATTACTT CCGTCTGAAC 180  
 TCAGACACGA GGACTTTAAT CGTTTGAACA AAGCAACCTT TAATAGCGGC TGCACCATCG 240  
 GGATGTCCTG ATCCAACATC GAGGTCGTAA ACCCTATTGT TGATATGGAC TCTAGAATAG 300  
 GATTGCGCTG TTATCCCTAG GGTAACTGT TCCGTTGGTC AAGTTATTGG ATCAATTGAG 360  
 TTTAGTAGTC CGCTTGGAGT GGTGAAGTCT AGAATGTCCT GTTCGGGGT TGGTTTCTGC 420  
 TCCAGGTGCG CCCCACCGA ATTTTTTATT GAAGTTGGG TAGTTTAGCA CCTGTGGGT 480  
 GTAAGGTAC TGTGGAATT AATAAATTA AGCTCCATAG GGTCTCCTCG TCTGTGTG 540  
 TAATGCCCC CTCTCCACGG GAAGGTCAAT TCCACTGTT AAAAGTAAGA GAAAGCTGAA 600  
 CCCTCGGGGA GCCATCCATA CAGGTCCCC 629

FIG.16K

## AD4-4 SP6 SEQUENCE

Sequence Range: 1 to 256

GCGGG TAAAT TGGTT TGTTA TTTTT TAAAA AAAAC TTGCA TGTTT AAAAA AAAGT TGATT 60  
 GCTTC AAATT TCTGC TACTA ACTTC AAGCT ATGGG AGTTT GGCAG TAGTC ACTTG AGGAT 120  
 TTTT TTCCA ATTCT TTTCT TTTTG TTGTT AAAGC TGTAC TTCAG TGAAC AGAAA AATTG 180  
 CCAAG CAAAC TAATG GACTA TAAAG CGTAA TTTGA CTGTG TGGGA CTAAC CTACA GAGCC 240  
 TACTT GACCA GTGGA T 256

FIG.16L

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AD4-4 T7F SEQUENCE

Sequence Range: 1 to 270

CATGT TTAAA AAAAA GTTGA TTGCT TCAAA TTA CTGCT TAACT TCAAG CTATG GGAGT 60  
TTGGC AGTAG TCACT TGAGG ATTTT TTTTC CAATT CGTTT TCATT TTTGT TGTTA AAGCT 120  
CGTAC TTCAG TGAGA CAGAA AAATT GCCAA GCTAA ACTAA TGGTC TATAA AAGCG TAATT 180  
TGCAT GTGTG GGCAA AACT ACAGA GCCTC AATTG CCACT GAGGT ATAGT ACAA GTTTT 240  
AATAC ATTTT GTAAA TCAAA TTGAA AGAAA 270

FIG.16M

AD4-4 SEQUENCE

CATGTTTAAA AAAAGTTGA TTGCTTCAAA TTA CTGCTAC TAACTTCAAG CTATGGGAGT 60  
TTGGCAGTAG TCACTTGAGG ATTTTTTTTC CAATTGTTT TCATTTTGT TGTTAAAGCT 120  
CGTACTTCAG TGAGACAGAA AAATTGCCAA GCTAACTAA TGGTCTATAA AAGCGTAATT 180  
TGCATGTGTG GGCAAAAAC ACAGAGCCTC AATTGCCACT GAGGTATAGT ACAAAGTTT 240  
AATACATTTT GTAAATCAAA TTGAAAGAAA 270

FIG.16N

AD16c-T7 SEQUENCE

TCTGC CCAGG CTGGT CTGAA ATTCC TGGGC TGAAG TGATC CTCCA GTCTT GGCCT CCCAA 60  
AGTGC TGGGA TTACA GGCAT GAGCT ACTGA GCCTA GCCTT AATGA TTAAT TTTAG AGTGA 120  
TGGCT TGTAC CTTCA AGACA CATAT AGATT GAGAC AGAAA ATTTC CATCG TCCCC GAGAA 180  
AACT 184

AD16c-T7 PEP

5 10 15 20 25 30 35 40 45 50 55 60  
SSSLG LPKCW DYRHE LLSLA LMINF RVMAC TFKQH IELRQ KISIV PRKLC CMGPV CPVKI  
65 70 75  
ALLTI NGHCT WLPAS

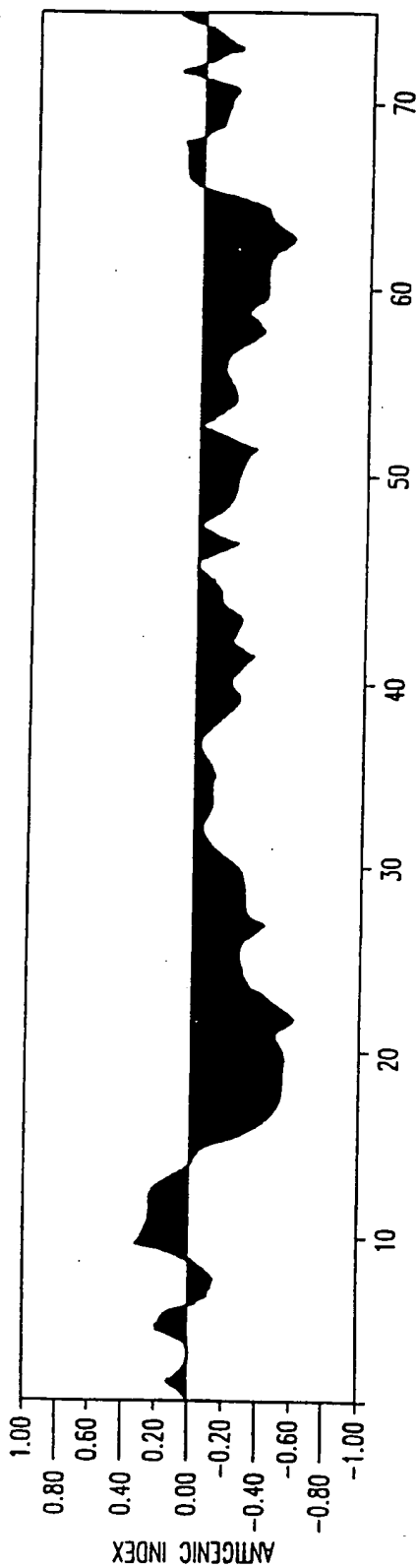
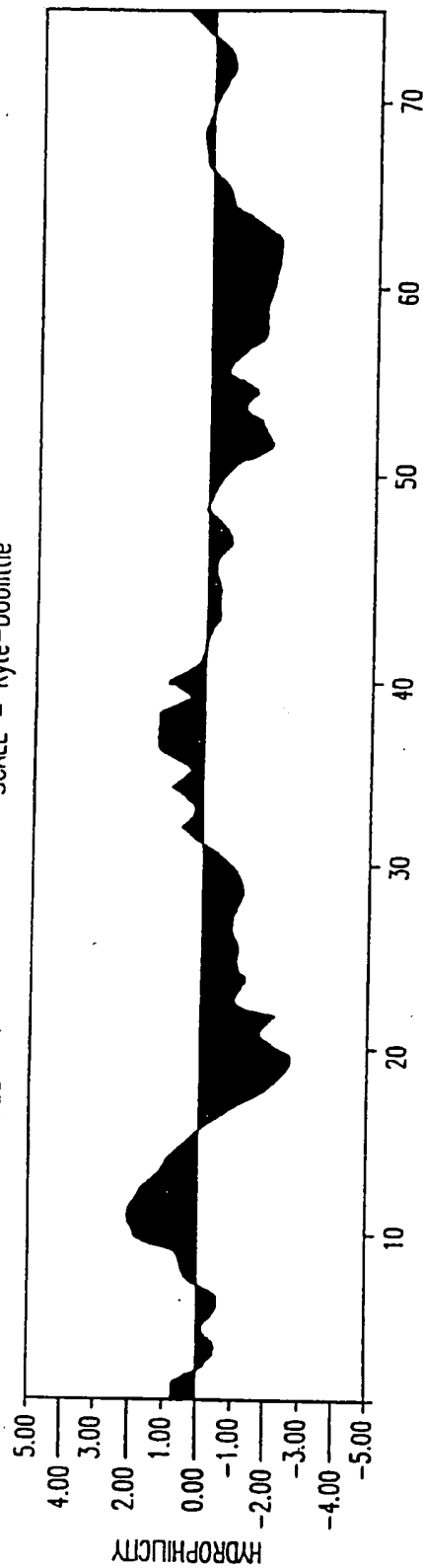
FIG.16O

SUBSTITUTE SHEET (RULE 26)

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AD16c 17 HYDROPHILICITY WINDOW PLOT

HYDROPHILICITY WINDOW SIZE = 7  
SCALE = Kyle-Doolittle



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## AD10-7 SEQUENCE

TTTTTTTTT GAGATGGAGT TTTGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT 60  
CTCAGCTCAC CGCAACCTCC GCCTCCCGG TTCAAGGAT TCTCTGCT CAGCCTCCCC 120  
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTAATT TTTTITAGTA 180  
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240  
TCCCGTCTCG GCCTGCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300  
TGCTCGCTA ATTTTGTGG TAGAAACAGG GTTCACTGA TGTGCCCAA GCTGGTCTCC 360  
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGTCAGCC 420  
GTGCTGGCC TTTTATTTT ATTTTITTA AGACACAGG GTACCACTCT TACCCAGGAT 480  
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540  
TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600  
TTTATTTTAA TTTTAAATT TTTGAGACAG AGTCTCACTC TGTACCCAG GCTGGAGTGC 660  
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCTCCCGG GTTCAAGTTA TTCTCTGCC 720  
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCAG CCTAGCTAAT TTTTGTAT 780  
TTTATAGTA GATGGGGTTT CACCATGTTT GCCAGTTGA TCTTGATCTC TTGACCTTGT 840  
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTGCTGACT CCACCGCGC 900  
CTATTTTAA TTTTGTITG TTTGAAATGG AATCTCACTC TGTACCCAG GTGGAGTGC 960  
AATGGCAAAT CTGGGCTACT CGCAACCTCT GCCTCCCGG TCAAGCGATT CTCCTGTCTC 1020  
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTT 1080  
CATTAGAGGC GGTTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140  
CCCACCTGCC TCAGCCTTCC AAAGTCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200  
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260  
TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320  
TTTAAACAG TTACATCTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAA 1380  
C 1381

FIG.16R

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## AD16c-SEQUENCE

CCATTGTTAG GTTGTCTCTT ACCTGTAAAT ATCAGGAGCT GACAAGAAAT GCTTACCACA	60
AAAGGAGAAA TGCCAGTCTA GTTAACAGTC AAGGAGAGAA ATCAGGAAGA TTATGTGGGT	120
GGAAGAAGTA GATGATGTGG CTGATGAGTG AGTGAGTGAG CAAGCCTCCG CCCAGCTGAA	180
GAAGGAGTCA GAACTGCCCT TTGTTCCCAA CTATTTGGCG AACCCAGCC TTCCCTTTTA	240
TCTATACACC CACAGCAGAG GATTACAGCC AGATGCAGAA TGGGGGCCCC TCCACACCCC	300
CTGCATCACC CCCTGCAGAT GGCTCACCTC CATTGCTTCC CCCTGGGAAC CTCCCCTGTT	360
AGGGACCTTT CCCCAGGACC ACACCTCTTT GGCAGTAGTT CAGAATGGTG ATGTGTGGC	420
CCCTCTGCCA TACTAGAACA CCAGAAAGAC AAACGGGTGA TGTITGTCAG CTACAGTGAG	480
TCTAGAGCCG TCCTGTTTTT TTCTGTCCCG TCCCAAGCCA CCATGTCTCT TCGAGCCTCA	540
AAATGGGACG TATGCAGGAC CAGCGCCAG ATTCCAAGCC ATTTTCTTC ACTGGAGCAT	600
TTCCATTTAA TATGCAAGAG CTGGTACTCA AGGTGAGAAT TCAGAACCCA TCTCTTCGAG	660
AAAATGATTT CATTGAAATT GAACTGGACC GACAGAGCTC ACCTACCAAG AGTTGCTCAG	720
AGTGTGTGC TGTGAGCTGG GTGTTAATCC AGATCAAGTG GAGAAGATCA GAAAGTTACC	780
CAATACTCTG TTAAGGAAGG ACAAGGATGT TGCTCGACTC AAGATTTTCAG GAGCTGGAAC	840
TGGTTCTGAT GATAGTGAAT ATAATTTTCT GTTCAGAAAT GCTGCATCAC ACTGACTGAA	900
AGGCCTTGCT ATACAGGAGA GCTTCAAAC TGACTTACTA ATGCAGCAGG GACTTTTATA	960
CTGAGTATAT GACAGTGTGC ATCAGCTCTG GGCCAAGGAC AAGCCATGAT CTAATGCCT	1020
CAGATGCCCC GGCCAGTCTG GTGCACTGCA TAGTATATAC GAACATCATT CTGCCCCAAG	1080
TAGGAAGCCC CATGACCCCC AAGCAGTGGT GTCCACTCTT CCAAGCCTCT TGGTGACAA	1140
TAAACCTTAT TGCTGAAGC TTTGAACGAC TGTGAGAATG GTCTGGCGAG GACGAGAACG	1200
TGGAATTATA TGAGTGTCTT TTGTATCCGA GAATGTAGAG AGTTCTCTGA AGACGACGAC	1260
TGAGAGAGAG CGGACGCTAT TTCTAGCCAC TCCTGTTCAG AGTGCACCTG AAGGGCTGGG	1320
ATGCGTTTTT CTGGTGTG CATGCTCACA ACTCTGCTGA CATTGGGAAC TTATGAGAGA	1380
GGAAGACTCG GGAAGCACA GATACTGGAC AGATCGATTC TGGTGTGGG AAAGCACAGA	1440
TACTGGACAG ATGGTTCTAG TGTGACTTGT GACTGTGAGG TTTCTATAA CATATTTATA	1500
AATGTTATC AGGTTCAAAA GTCTATAAGA ATACAGTTCC AGACTGAAT GCTTCGAAAT	1560
ACTTCGATGT TGGGAACCAA AAGAGCTTTC CCTCCCTCAC TTTTCTTT GTAACACTCA	1620
TGACTGCTTC TCTGTCTCGA GTCATCTCTG CATTAACTCC CCTTCGTGGT CACTAGAGGG	1680
CTCTCTGATG CTTCTAAGAC ACTGCTTTTT ACATGCCACA CCCACGCGT AGACACAGGG	1740
TCTCACTATG TGGCCCAGGC TGGTCTCAA CTTCTGGCCT TAAGTGATCG TCCTGTCTTT	1800
CGCGCTCGGA AGAAAGTCGT GGGGATTACA GGTGTGAGCC ACCCGCCAG CCCCTCCCTT	1860
GTGTTTCAAC CAATCGGAAG TGAATTTAAC TAGATGTACT AACCTTTTTT TTCTTTGACT	1920
TCTAAAAAAG TTACAGTTTA CTAATAAAGT TAAGTCTGGT TCTGTCTAG AGGAAATAAA	1980
TTCACTATTA ATTCATGTCT TAAGTTACTT GGGTTAAAC ACTTTCAGCC ACCCAGATTA	2040
ATTAAAGTGC AGCAGTGGAG CCCCTGGCTG GGGAGATGGG CCTCCAGAGG AGCAGCTGCA	2100
GGCATGTTCT GGCTACACAG AGGCAAGCAA GGGACTGGTG TCTCTGGTGA GAGGTGGGT	2160
TGATGTATCT CTGTCTATG CTGGTCTCTC TTCTCCTTTA TAAATCCTCC TGTGGTCACT	2220
GACTATCGTA TCGCAGTGAT CAGACTGCAC ATAGTACGGT TAGGCTGAGC TTAATGTCTT	2280
AATCATGTCA TTCGAGAGAA GACACGTTTT GATTCATGCT TTGTGTAATT AATCAATCAA	2340
GGATTCTTTT TTAGCTTTG TTGACGTGTA ATTCACCCCT CCTCCTCCAC TGCATATTTA	2400
AAGCATGTGT TCACACTGTG TGTATACATT CACTGOGATT TTTTGGTTG CTGCATTGCT	2460
TGGACTGTTT ATAACATCAC AAGTATTATT CAAATAAAAT ATTAAGTAC CGAAAAAAA	2520

FIG.16S

SUBSTITUTE SHEET (RULE 26)

H REG GENE		5	10	15	20	25	30	35	40	45	50
[ 220 ]	GA	ALTCC	TGggC	TCAaG	TGATC	ClCtC	atgTC	AGlCT	CCCAA	ACTGC	TGGGA>
AD2-283	GA	ACTCC	TGACC	TCAGG	TGATC	CGCCC	GCCTC	AGCCT	CCCAA	ACTGC	TGGGA

H REG GENE	55	60	65	70	75	80	85	90	95	100	
[ 220 ]	TgACA	gGCtT	G-AG-	CC-A	-CCAc	ACcAg	gcccc	-TC-	AlCa-	G-tT	tTtAT
AD2-283	TTACA	AGCGT	GCAGA	COGCA	CCCAG	ACGAT	TTTAA	TTCTT	AACNT	GCCAT	CCTCT

H REG GENE	105	110	115	120	125	130	135	140
[ 220 ]	AGaAa	AaAaa	ACcTT	AaaaT	tgltA	gCAAA	lacta	tGACA>
AD2-283	AGTAC	AGACC	ACTTT	AGTGT	CCCTA	TCAAA	GGGGG	AGACA

FIG.17

RAT PTP 605  
[ 144 ] <ACTC  
AD2-2 T7 ACTC

RAT PTP            710    705    700    695            690    685            680            675            670    665  
[ 144 ]    <CA-T   oCAAT   AoTGg   oGaLA   -aaaa   ToCcA   T-A-G   GgCag   T-GA   GGcA-   AgaaT   GTTIG  
AD2-2 T7   TCATT   TCAAA   ATTGC   TGCCA   GTGTT   TTCAA   TGATG   GACAA   TCAGA   GGGAT   ATGCT   GTTAG

RAT PTP  
[ 144 ]  
AD2-2 T7

745 740 735 730 725 720 715  
<GTg A-Agg taTTT TTaT TaaaT gTgca gggTT  
GTA ATACT CCTTT TTTCT TCTTT CTTTT TTTTT

5  
FVF cLII>  
HPTPAA FVA SLIK

FIG. 17A

**SUBSTITUTE SHEET (RULE 26)**

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1-9aT7-3 3 140 145 150 155 160 165 170 175 180 185 190 195  
 [ 206 ] ACcAC GCCCc GCTAA TTTTT GTATT TTTAG TAGAG AcdGG GTTTC aCCgT GTTgg cCAGG>  
 AD2-283 ACAAC GCCCA GCTAA TATTT GTATT TTTAG TAGAG ATGGG GTTTC TCCAT GTTCA TCAGG

1-9a-T72 3 15 20 25 30 35 40 45 50 55 60 65 70  
 [ 260 ] CTGGT cTgaA ALTCC TGggC TgAoG TGATC ClCCa GtCTl gGCCT CCCAA AGTGC TGGGA>  
 AD2-283 CTGGT GTCGA ACTCC TGACC TCAGG TGATC CGCCC GCCTC AGCCT CCCAA AGTGC TGGGA

1-9a-T72 3 140 145 150 155 160  
 [ 260 ] AG-AC AcA-t A-Tag ALTGo gaC-A gaAAA>  
 AD2-283 AGTAC AGACC ACTTT AGTGT CCCTA TCAAA

## FIG.17B

AD16c-SP6  
 [ 344 ]  
 AD2-2 SP6

5 10 15 20 25 30  
 —AGA— TcTCg CTC-T G-Tca CCCAG GCTGa AGTGC>  
 AGAG TTTCA CTCTT GCTTG CCCAG GCTGG AGTGC

AD2-2 SP6 35 40 45 50 55 60 65 70 75 80 85  
 [ 344 ] AgTGG CcCAA TCleG GCTCA CTGCg AgCTC C-aCC TCCCG gGltC Actlc aTTCT CCTGC>  
 AD2-2 SP6 AATGG CACAA TCCTG GCTCA CTGCA ACCTC CGCCC TCCCG AGCTC AAGAA CTTCT CCTGC

AD16c-SP6 100 105 110 115 120 125 130 135 140 145 150 155 160  
 [ 344 ] CTCAG CCTC- TGAGl aGCTG GGAcT ACAGG CGCcC aCCAC AcGCc gCTAA TTTTT GTATT>  
 AD2-2 SP6 CTCAG CCTCG TGAGC CGCTG GGATT ACAGG CGCGC GCCAC AAGCG ACTAA TATTT GTATT

AD16c-SP6  
 [ 344 ] TTTGT AG>  
 AD2-2 SP6 TTTGT AG

AD16c-SP6 140 145 150 155 160 165 170 175 180 185 190 195  
 [ 206 ] ACcAC GCCCc GCTAA TTTTT GTATT TTTAG TAGAG AcdGG GTTTC aCCgT GTTgg cCAGG>  
 AD2-283 ACAAC GCCCA GCTAA TATTT GTATT TTTAG TAGAG ATGGG GTTTC TCCAT GTTCA TCAGG

AD16c-SP6 200 205 210  
 [ 206 ] aTGcT —CGA lCTCC TGA>  
 AD2-283 CTGGT GTCGA ACTCC TGA

## FIG.17C

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H REG GENE 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660  
 [ 118 ] —CC CC-aa gC-aG lGTta aTccI GG-cT A-CT GlgTG AGcTG AccTC AagcA CoGGt>  
 AD3-4 CC CCTGT TCTTG GGTGG GTTTC GGTAT ATTCT GGTTC AGATG ATATC ATTTA CCGGG

H REG GENE 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720  
 [ 118 ] GAAGG Cagag aaTcc A-Tcc aCC-T gTTTC TgTTc TCCcT gCtTA gctcc AGGga TgGAA>  
 AD3-4 GAAGG CGCTT TGTGA AGTAG GCCTT ATTTC TCTTG TCCTT TCGTA CAGGG AGGAT TTGAA

H REG GENE 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770  
 [ 118 ] cTgGg Actgg GoT-a gAgga aaG-g TGAAC TC-cT CA-lT aagga aATgG aTG>  
 AD3-4 GTAGT AGAAC GCTGT TACTC CCGTC TGAAC TCACT CACGT GGCTT TATCG TTG

FIG.18

WPO3-5 T7 5 15 20 25 30 35 40 45 50  
 [ 90 ] GATCC aAGCT acGTA -CgcG TgcAT GCACg lCaTa gcTcT TCTAT AGTGT CAC>  
 AD3-4 221 GATCC GAGCT CCGTA CCAAG TTGAT GCATA GCTTG AGTAT TCTAT AGTGT CAC

18-4T7 155 150 145 140 135 130 125 120 115 110 105  
 [ 362 ] <gTATg GgCcc gATAg —c-l TAT-l TAgcC TTTAG AGCAC ACTGG CgGCC GTTAC TAGTG  
 AD3-4 221 ATATA GACAA TATAA CAATA TATTG TATAC TTTAG AGCAC ACTGG CAGCC GTTAC TAGTG

18-4T7 100 95 90 85 80 75 70 65 60 55 50 45  
 [ 362 ] <GATCC GAGCT CCGTA CCAAc TTGAT GCATA GCTTG AGTAT TCTAT AGTGT CACcI -aAoT  
 AD3-4 221 GATCC GAGCT CCGTA CCAAG TTGAT GCATA GCTTG AGTAT TCTAT ACTGT CACTA ATAGT

FIG.18A

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G2A-EP T7 20 25 30 35 40 45 50 55  
 [ 148 ] ——— CTT AaTA- gAlAg cLaCT TA— AAAla AcTTA CoC-A cT— GTtTt>  
 AD3-4 SPF CTT ACTAC CAGAC AACCT TAGCC AAACC ATTTA CCCAA ATAAA GTATA

G2A-EP T7 60 65 70 75 80 85 90 95 100 105 110  
 [ 148 ] aGdG- T-G— cTTGA AAaCT aLClg AlcAG AcATA GTAll GaAAc cAAIG A—Al AcATT>  
 AD3-4 SPF GGCGA TAGAA ATTGA AACCT GGCGC AATAG ATATA GTACC GCAAG GAAAG ATGAA AAATT

G2A-EP T7 115 120 125 130 135  
 [ 148 ] AT-Al aAAG- -TAA- A-gGo AAGGA -gAA>  
 AD3-4 SPF ATAAC CAAGC ATAAT ATAGC AAGGA CTA

AD3-4 215 210 205 200 195 190 185 180  
 [ 182 ] ——— <CT ATAAa GgTcG TTG— TcaaC gaTaa AGCAc GtGAc  
 H REG GENE CT ATAGA GATTG TTGAT TTGCC TCTTA AGCAA GAGAT

AD3-4 175 170 165 160 155 150 145 140 135 125  
 [ 182 ] <TgAgt lCAG- aCcGg A-Gta aCAG- CgLLC TacTA CTTCA -aaTc cTC-C CTGCg aaAgG  
 H REG GENE TCATT GCAGC TCAGC ATGGC TCAGA CCAGC TCATA CTTCA TGCTG ATCTC CTGCC TGATG

AD3-4 120 115 110 105 95 90 85 80 75 70 65 60  
 [ 182 ] <caaga Gaaat AagGC ClAct TAAGc gC-CT TccCC cglAA olgAl alcaT CTcaa CCaGA  
 H REG GENE TTTCT GTCTC AGAGC CAAGG TAAGA TCTCT TTTCC ACCAA CCAAC TCTTT CTAGC CCTGA

AD3-4 55 50 45 40 35 30 25 20 15 10  
 [ 182 ] <AlA-T aCcCa aaccC CCCAA GaAcA gGGGa ggAaa aGAAA AAAAA AAAAA  
 H REG GENE AGACT TCACT CTATC CCCAA GCATA CCGGT CTACT TGAAA AAAAA AAAAA

FIG.18B

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AD2-2 T7		535	530	525	520	515	510	505	500	495
[ 110 ]	—————	CAGAA	AACto	GCTAc	oC-AA	tgcAt	TGGTC	TATcA	tglla	oAAcg
AD4-4 T7F		CAGAA	AAATT	GCCAA	GCTAA	ACTAA	TGGTC	TATAA	AAGCG	TAATT

AD2-2 T7	490	485	480	475	470	465	460		
[ 110 ]	<TGCAT	-T—o	GoCAc	AAA-T	ACAoA	oacCA	TG—A	-AacA	oGCcA
AD4-4 T7F	TGCAT	GTGTG	GGCAT	AACT	ACAGA	GCTCA	TGCTA	GAGTA	TGCAA

1-9o		145	140	135	130	125	120	115	110		
[ 142 ]	—————	<AA	-TTGg	gToC-	-Cggg	cccCc	cCTA-	gAggT	cgAcG	gTAT-	cGA-T
AD4-4 T7F		AA	GTTGA	TTGCT	TCAA	TTTCT	GCTAC	TAACT	TCAAG	CTATG	GGAGT

1-9o	105	100	95	90	85	80	75	70	65	60	55	50
[ 142 ]	<oogct	lGTAl	cgAoT	TccGG	AcTTT	gcTT-	—TT	gGTTT	TCcTT	Tcctg	TGaaA	AgGtT
AD4-4 T7F	TTGGC	ACTAG	TCACT	TGAGG	ATTTT	TTTTc	CAATT	CGTTT	TCATT	TTTGT	TGTTA	AAGCT

1-9o	45	40	35	30	25	20	15	10		
[ 142 ]	<gGTlt	TaaAG	TGAG-	-AtAc	ActTT	tCC—	GlagA	ACoAg	TGtTC	TAT
AD4-4 T7F	CGTAC	TTCAG	TGAGA	CAGAA	AAATT	GCCAA	GCTAA	ACTAA	TGGTC	TAT

FIG.19

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H REG GENE		5	10	15	20	25	30	35	40	45
[ 278 ]	g	AATTC	CTGGG	CTcAA	GTGAT	CCTCt	coTgT	coGtC	TCCCA	AAGTG>
AD16C-T7-A	A	AATTC	CTGGG	CTGAA	GTGAT	CCTCC	AGTCT	TGGCC	TCCCA	AAGTG

H REG GENE	50	55	60	65	70	75	80	85	90	95	100	105
[ 278 ]	CTGGG	ATgAC	AGGCl	TGAGC	cACcA	caCCa	gcCCa	TcATc	AgTtt	TTaTA	tAaAG	-aaaa>
AD16C-T7-A	CTGGG	ATTAC	AGGCA	TGAGC	TACTG	AGCCT	AGCCT	TAATG	ATTAA	TTTTA	GAGTG	ATGGC

H REG GENE	110	115	120	125	130	140	145	150	155	160		
[ 278 ]	aaaaA	CCT-t	A-aA	AltgI	TA-gG	caaAl	AaLGA	cAAaT	TgtAa	ta-lo	tattc	ttACa>
AD16C-T7-A	TTGTA	CCTTC	AAGCA	ACATA	TAGAG	TTGAG	ACAGA	AAATT	TCCAT	CGTCC	CGAGA	AAACT

H REG GENE	165	170	175	180	185	190	195	200	205	210	215	220
[ 278 ]	LTlCa	-gATl	tlLat	tlTlT	aaaCT	GAaAA	GAatt	gatTA	aTAAa	TaAAA	LTtaG	LAT-->
AD16C-T7-A	GTGCT	GCATG	GGCCC	CGTGT	CCCCT	GTGAA	GATCG	CCCTA	TTAAC	TATAA	ATGGG	CATTG

H REG GENE	225	230	235	
[ 278 ]	t-aA-	-tcTG	t-clt	TTaA>
AD16C-T7-A	CACAT	GGTTC	CCAGC	TTCA

FIG.20

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AD16C  
[ 266 ] \_\_\_\_\_ 5 10 15 20  
Human-PTP aACgt TtcGA oCCTo lCgTg>  
TACTG TGTGA GCCTG ACCTC

AD16C 25 30 35 40 45 50 55 60 65 70  
[ 266 ] AAG-c -ccGA TTtla GAgtT ootAc -ggGT -gC- lTcAA GggA- acggg gCToT -ga->  
Human-PTP AAGCA CAGGA TTCCA GAAAT GGAAG GATGT GCCTT GTGAA GACAA GTTCT CCTTT GTCTG

AD16C 75 80 85 90 95 100 105 110 115 120 125 130  
[ 266 ] gAAGT -tttc lACgg GgoGC -oTG GAAAt TttcT GTCTc oAtaT GtgCl lGoAg gTACA>  
Human-PTP CAAGT TCAAA AACTA GAGGC AGCTG GAAAA TACAT GTCTA GAACT GATCC AGCAA TTACA

AD16C 135 140 145 150 155 160 165 170 175 180 185 190  
[ 266 ] ACcGt oTClA AAATT AAlCa tt-aa ggCTa ggCtc agtAg CTClg CCTGt -o-oT CcCag>  
Human-PTP ACGGA GTCAA AAATT AAACC GGACC ATCTC TCCAA CTCAA CTCAA CCTGG ACACT CTCTT

AD16C 195 200 205 210 215 220 225 230 235 240  
[ 266 ] CaC-t lTcgG gagGC Coo- gAcTg gaggA TcacT TcAg- ccCag gAa-t TTcoG AcgCc>  
Human-PTP CTCTG CTGAG TTTGC CTTGT TAATC TTCAA TAGTT TTACC TACCC CAGTC TTTGG AACCT

AD16C-T7-A 205  
[ 33 ] \_\_\_\_\_ VPCE Dr>  
HPTPAA VPCE DK

RPTP AA 115 120  
[ 33 ] SgSLf LyKsW D>  
Translatio SSSLG LPKCW D

FIG.20A

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## ALIGNMENT OF AD16C-SP6 cDNA WITH AD2-2 SP6 cDNA

AD2-2 SP6 40 45 50 55 60 65 70 75 80 85 90  
 [ 362 ] CTtGC T-TG- —CCC AGGCT GgAGT GCAaT GGCaC AATCc LGGCT CACTG CcAcC TCCcC>  
 AD16C-SP6- CTCCG TCTGT CACCC AGGCT GAAGT GCAGT GGCCC AATCT CCGCT CACTG CGAGC TCCAC

AD2-2 SP6 95 100 105 110 115 120 125 130 135 140 145  
 [ 362 ] CTCCC GcGcT CAaga acTTC TCCTG CCTCA —GCC TC-G- —TG AGccG CTGGG AITAC>  
 AD16C-SP6- CTCCC GGGTT CACTT CATTG TCCTG CCTCA CTGCC TCAGC CTCTG AGTAG CTGGG ACTAC

AD2-2 SP6 150 155 160 165 170 175 180 185  
 [ 362 ] AGGCG CgCgC CA-CA aG— -CgaC TAA-T aTTTG TATTT TT-GT AG>  
 AD16C-SP6- AGGCG CCCAC CACCA CGTCC CCTGC TAATT TTTTG TATTT TTAGT AG

AD2-283 50 55 60 65 70 75 80 85 90 95 100 105  
 [ 374 ] CCoTG TTcaT CAGGc TGGTg TCGAa CTCCT GACCT CGTGA TCCGC CCGCC TcAGC ClCCC>  
 AD16C-SP6- CCGTG TTGGC CAGGA TGGTC TCGAT CTCCT GACCT CGTGA TCCGC CCGCC TTGGC CACCC

AD2-283 110 115 120 125 130  
 [ 374 ] AAAGt G-cTG GGATT ACAaG CGTGC>  
 AD16C-SP6- AAAGA GTTTG GGATT ACAGG CGTGC

FIG.20B

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AD3-4

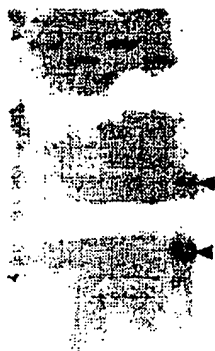


FIG. 21A

AD2-2



FIG. 21B

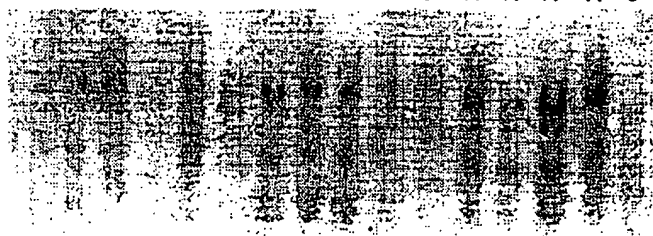
AD3-4



FIG. 21C

AD3-4 CLONE

C C C C A C A A C C C A A A A C



—185

C C C C A C A A C C C A A A A C

#27 NORTHERN

FIG. 21D

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## G2-2Pst-M13F SEQUENCE

Sequence Range: 1 to 251

```

TGCAG CAATG GCAAC AACGT CTGCA AACTA TTAAC TGGCG AACTA CTTAC TCTAG CTTC 60
CGGCA ACAAT TAATA GACTG GATGG AGGCG GATAA AGTTG CAGCA CCACT TCTGC GCTCG 120
GCCCT TCCGG CTGGC TGGTT TATTG CTGAT AAATC TGGAG CCGGT CGAGC GTGGG TCTCG 180
CGTAT CATTG GAGCA CTGGG GCCAG ATGGT AAGCC CTCGG TATCG TAGTT ATCTC ACAGC 240
AGGGA GTCAG G
251

```

FIG.22

## G2-2Pst-M13R SEQUENCE

Sequence Range: 1 to 242

```

TGCAG GAGCG GGGAG GCAAG ATGGC CGCTT TGGTC CGGAT CTTTG TGAGG AACCT TACTT 60
CTGTG GTGTG ACATA ATTGG ACAA CTACC TACAG AGATT TAAAG CTCTA AGGAA ATATA 120
AAATT TTTAA GTGTA TAATG TGTTA AACTA CTGAT TCTAA TTGTT TGTGT ATTTT AGATT 180
CCAAC CCTAT GGAAC CTGAT GAATG GGAGC CAGTG GTGGA ATGCC TTTAA TGAGG AAACC 240
TG
242

```

FIG.22A

## G2-2Pst1-EcoR1-M13F SEQUENCE

Sequence Range: 1 to 208

```

TGCAG CAATC TTTCT TATAT ACATG CTTAA TAGAT AGCTA CTTAA AATAA CTTAC ACAAG 60
TTTTA GAGTT GCTTG AAAAC TATCT GATCA AGACA TAGTA ATTGA AACCA ATGAA TACAT 120
TATAT AAAGT AAAGG AAAGG AGAAG AGAGG AAAGG GAGGG GAAGA GGAGA GGGAG GGACA 180
AGCGA GAAAG GAAAG GGAAG GGAGA AAA
208

```

FIG.22B

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## Gen2-2PstI-EcoRI-M13R SEQUENCE

Sequence Range: 1 to 152

```
CTCAC TAAAG GGATC AAGGA ATAAT TTTGA ATTC AAGTC TTACA TTAA TAAAT ACATT 60
CATAA GGCTA TAACT ACCAT ACGTT GTGAT TTCTC TGATT AATTT AAAAA TAAAT TAAAA 120
CCTGG AAAGA ATTTT ACCAT TCTAG GAAGC CA 152
```

## FIG.22C

## G2-2PstI-EcoRI-T7 SEQUENCE

Sequence Range: 1 to 338

```
AATCT ATCTT ATATA CATGC TTAAT AGATA GCTAC TTAAA ATAAC TTACA CACGT TTTAG 60
AGTTG CTTGA AAAC TCTG ATCAA GACAT AGTAA TTGAA ACCAA TGAAT ACATT ATATA 120
AAGTA AAGGA AAGGA GAAGA GAGGA AAGGA GGGGA GAGGA GAGGA GGACA AGCGA GAAAA 180
GGAAG GGAAG GGAGA AAAAG GGGGA AAGGG AGGTA GAGAG AGAGA GAAAA AGTGC TGGTC 240
ATATA GTAAG TGTAC ATTTT AACTT TTAA GAAAC TACCC TACTC TATTC CAGAG TGATT 300
GTACA TGTGC ATTTT ACTGC ATTAT AGAGA TCATT TTC 338
```

## FIG.22D

## G5dPstI-M13R SEQUENCE

Sequence Range: 1 to 169

```
TGCAG GAGTC GGGAG GCACG ATGGC CGCTT TGGTC CCGAT CTTTG TGAAG GAACC TTAAT 60
TCTGT GTGTG ACATA ATTGG AAAAA CTACC TACAG AGATT TAAAC GTCTA AGGTA AATAT 120
AAAAT TTTTA GTGTA TAGGT TAAAC TACTG ATTCT AATGT TGTGT ATTT 169
```

## FIG.22E

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## G5d Pst-T71 SEQUENCE

Sequence Range: 1 to 209

```

CCCCG GGCTG CAGCA ATGCG AACAA CGTCT GCAAA CTATT AACTG GCGAA CTCAT TCATC 60
TAGCT TCCCG GCAAC AATTA ATGAC TGGAT GGAGG CGGAT AAAGT TGCAG GACCA CTTCT 120
CGCGT GGCCC TTCOG GCTGG CTGGT TTATT GCTGA TAATT GAGCG TGCGA GTGGC TCGCG 180
TATCA TTCCG GACAT GGGCC AGTAG GTAC                                     209

```

FIG.22F

## G5dPst1-EcoR1-SP SEQUENCE

Sequence Range: 1 to 272

```

CTTGC CCTTC ATGGA GTCAT ACAGC CGATC AGCAA AATGC AGGGG CTGTG TCTGA ATGCA 60
CTGAA CCAGG TTCAG GAAAG CATTT TCCAG GTCTC CTTTA ACCTC TTTCC TGATG CTTTC 120
CAACA TGTC AAGG GCTGT AACTC TTGTA CCTAT CAAAT ACTTT CTGGA GGTGG GGACA 180
CGCTC CGCTC GGTCA TGATG CTGAT CCACT TGGGA ACATC AGTTC TTTCC TCTTC ACTCC 240
AGCTG CATAG AGATC CCAGG ACTCT TGGTC AA                                     272

```

FIG.22G

## G5dPst1-EcoR1-t7 SEQUENCE

Sequence Range: 1 to 278

```

ACGGC CCAGC TTCCT TCAAA ATGTC TACTG TTCAC GAAAT CCTGT GCAAG CTCAG CTTGG 60
AGGGT GATCA CTCTA CACCC CCAAG TGCAT ATGGG TCTGT CAAAG CCTAT ACTAA CTTTG 120
ATGCT GAGCG GGATG CTTTG AACAT TGAAA CAGCC ATCAA GACCA AAGGT GTGGA TGAGG 180
TCACC ATTGT CAACA TTTTG ACCAA CGCA GCAAT GACAC GAGAC AGGAT ATTGC CTTCC 240
CCTAC CAGAG AAGGA CCAAA AAAGG AACTT GCATC ACA                                     278

```

FIG.22H

ALIGNMENT OF G2-2Psl1 with HUMAN REG GENE (1)

EXONS	100	105
[ 124 ]	AcTGl	GTgAG>
G2-2Pst-Mo3F	AGGGA	GTCAG

FIG. 23

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## ALIGNMENT OF G2-2Pst with HUMAN REG GENE (2)

H REG GENE 3155 3160 3165 3170 3175 3180 3185 3195 3200  
 [ 194 ] —AG GAGac tTGtG GlA-a AaaLC tGCTg cIGTa ClGcT CoTT- TG-GG AACCT TA-gT>  
 G2-2Pst-M13R AG GAGCG GGGAG GCACG ATGCC CGCTT TGGTC CCGAT CTTTG TGAGG AACCT TACTT

H REG GEN3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265  
 [ 194 ] aTact aaaTa AlATA A-Tat AlcAA CoACT aAlgG lcAgc cAAlG CTaTg cIG-g ATATg>  
 G2-2Pst-M13RCTGTG GTGTG ACATA ATTGG ACAA CTACC TACAG AGATT TAAAG CTCTA AGGAA ATATA

H REG GENE 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320  
 [ 194 ] AgggT ccT-g GgccA cAAaG acaaA AAaT- CoGga aCcAc TT-TT TaaGT gagaT AcTTT>  
 G2-2Pst-M13RAAATT TTAA GTGTA TAATG TGTTA AACTA CTGAT TCTAA TTGTT TGTGT ATTTT AGATT

H REG GEN3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375  
 [ 194 ] gggLC tCTgT -cAAa lTcAT aAcac lTalt lclTG GTGGA ATaCa gTTAA TGAG>  
 G2-2Pst-M13RCCAAC CCTAT GGAAC CTGAT GAATG GGAGC CAGTG GTGGA ATGCC TTAA TGAG

G2-2Pst-Ma3F 150 155 160 165 170 175 180 185 190 195  
 [ 130 ] —TA aAlCl GgaGC cGG— -TcGA GC-GT GGGTC tCgcG TaTCo TlCga GcaCT>  
 EXONS TA GAACC GCCGC TGGCA CTGGA GCAGT GGGTC CCTGG TCTCC TACAA GTCCT

G2-2pst-M13F 200 205 210 215 220 225 230 235 240 245 250  
 [ 130 ] GGGGC —caG A-lgg tAAGC ccTcc gTATC gTcGt TA-Tc TcacA GCagG gagTC AgG>  
 EXONS GGGGC ATTGG AGCCC CAAGC AGTGT TAATC CTGGC TACTG TGTGA GCCTG ACCTC AAG

FIG.23A

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## ALIGNMENT OF G2-2PST-ECOR1-T7 WITH HUMAN REG GENE

H REG GENE		335	340	345	350	355	360	365
[ 132 ]	_____	AT	AGATA	tCTAC	TTlAl	lcgAl	TTAaA	tlCTG -TTTA>
G2-2PST-ECOR1 T7		AT	AGATA	GCTAC	TTAAA	ATAAC	TTACA	CACTG TTTTA

H REG GENE	370	375	380	385	390	395	400	405	410	415
[ 132 ]	-GTa	lTTlA	tlA-T	ATlTl	gTlA-	A--T-	ccAlT	TG-lc	CCAAT	lcATA lAcT- TAT>
G2A-EP T7	GAGTG	CTlGA	AAACT	ATCTG	ATCAG	ACATA	GTAAT	TGAAA	CCAAT	GAATA CATTa TAT

RAT PTP		740	735
[ 82 ]	_____	<TqAAq	qtATT
G2-2PST-ECOR1-M1			TAAAT
ACATT			

RAT PTP	730	725	720	715	710	705	700	695	690	685
[ 82 ]	<-Tlt	allTA	-AAtg	tgCA-	ggGTT	-acA-	TaCaa	TaATg	gAgaT	AAAAA TAcca TAggg
Gen2aEP-Ma	CATAA	GGCTA	TAACT	ACCAT	ACGTT	GTGAT	TTCTC	TCATT	AATTT	AAAAA TAAAT TAAAA

RAT PTP	68675	670	665	660	655
[ 82 ]	<CgaGG	caAGA	ATgTT	—lg	TCTAG GAAG
G2-2PST-ECOR1-M1	CCTGG	AAAGA	ATTTT	ACCAT	TCTAG GAAG

FIG.23B

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Human-PTP		270	280	285	290	295	300	305	310	315		
[ 166 ]	—	AcCTG	GtGct	gTgCT	cAC-C	cAGgc	cgaGG	gtgC-	cTTlg	TgGcC T-cAc	IGAll>	
G5dPst-l		AACTG	GCGAA	CTACT	TACTC	TAGCT	TCCGG	CAACA	ATTAA	TAGAC	TGGAT GGAGG	
Human-PTP	320	325	330	335	340	345	350	355	360	365	370	
[ 166 ]		aaG-g	AgAGT	gGCAl	GAtgA	CTTCa	aTG-T	CtG-g	aTT—	GGC—	-CTcc	aTgAc ccCaa>
G5dPst-l		CGGAT	AAAGT	TGCAG	GACCA	CTTCT	GCGCT	CGGCC	CTTCC	GGCTG	GCTGG	TTTAT TGCTG
Human-PTP	375	380	385	395	400	405	410	415	420	425	430	435
[ 166 ]		AaAgA	aCcGc	cGClG	GgGAG	CGTGG	GTCcC	tgGTc	TCcTa	caAGt	cCTGG	GG-CA -LTGG>
G5dPst-l		ATAAA	TCTGG	AGCCG	GTGAG	CGTGG	GTCTC	GCGTA	TCATT	GCAGC	ACTGG	GGCCA GATGG
Human-PTP		440	445	450	455	460	465	470				
[ 166 ]		—AGC	CCcaa	GcA—	GTGtT	aATCc	tggCt	AClGt	GtG-A	-GcC>		
G5dPst-l		TAAGC	CCTCC	GTATC	GTGGT	TATCT	ACACG	ACGGG	GAGTA	CGGC		

FIG.23C

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H REG GENE 80 85 90 95 100 105 110 115  
 [ 158 ] ————— AG GC-Cc ATcat CagTT T—T- tatAT aaaga aaAAa oAACC TTAaa>  
 G5dPst-M AG GCACG ATGCC CGCTT TGGTC CGGaT CTTTG TGAAG GAACC TTACT

H REG GENE 120 125 130 135 140 145 150 155 160 165 170 175  
 [ 158 ] atTGT taGgc AoATA cTatG ACAA -Ttgt aAtat ALATT cttAC aTtTc AGaT- -tTtT>  
 G5dPst-M TCTGT GTGTG ACATA ATTGG ACAA CTACC TACAG AGATT TAAAC GTCTA AGGTA AATAT

H REG GENE 180 185 190 1195 200 205 210 215 220  
 [ 158 ] Atllt TTaaA cTGTA TAGaa TlgAt TAaTa AoTaa AAT-T T-aGT ATT>  
 G5dPst-M AAAAT TTTTA GTGTA TAGGT TAAAC TACTG ATTCT AATGT TGTGT ATT

G5dPst-l 125 130 135 140 145 150 155 160 165  
 [ 118 ] ————— TA aAtCl GgaGC cCG— -T-GA GC-GT GGGTC tCgcG TaTca TtgcA GcaCT>  
 EXONS TA GAACC GCCGC TGGCA CTGA GCAGT GGGTC CCTGG TCTCC TACAA GTCCT

G5dPst-l 170 175 180 185 190 195 200 205 210 215 220  
 [ 118 ] GGGGC —caG A-lgg tAAGC ccTcc gTATC gTGGl TA-Tc T-acA —cG ACggg gAGlA>  
 EXONS GGGGC ATTGG AGCCC CAAGC AGTGT TAATC CTGGC TACTG TGTGA GCCTG ACCTC AAGCA

G5dPst-l  
 [ 118 ] C-GG>  
 EXONS CAGG

FIG.23D

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FIG. 24A

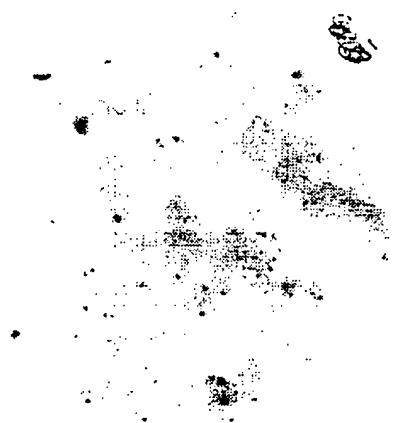


FIG. 24B

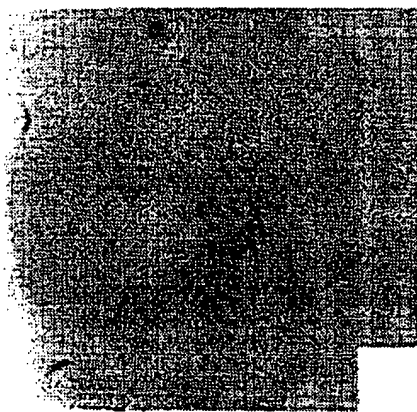
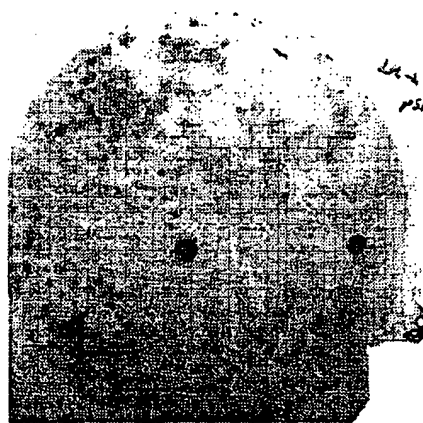


FIG. 24C

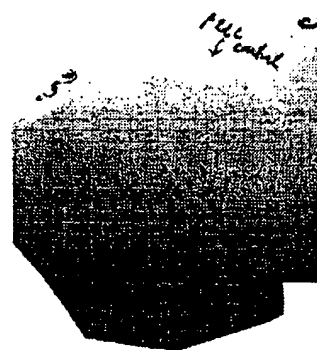


FIG. 24D

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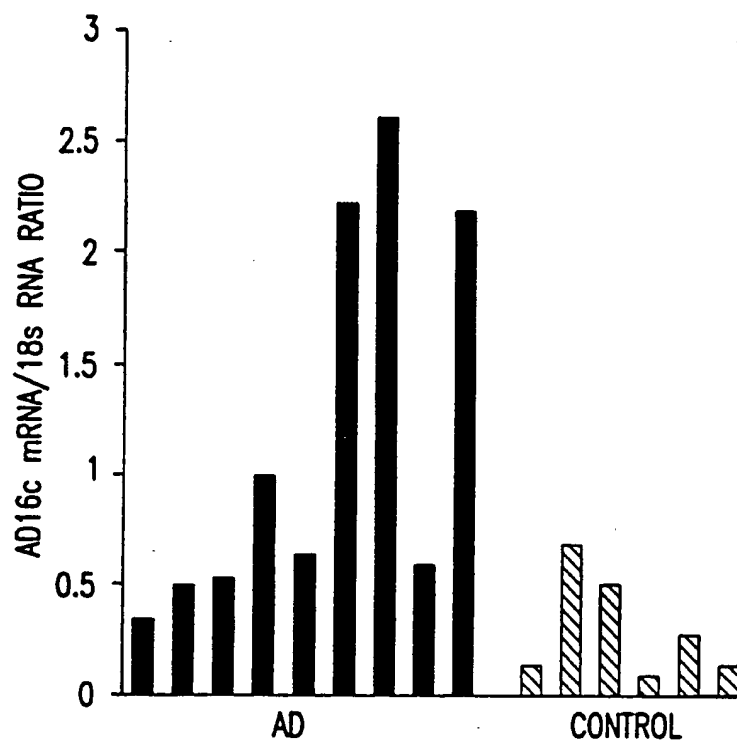


FIG. 25A

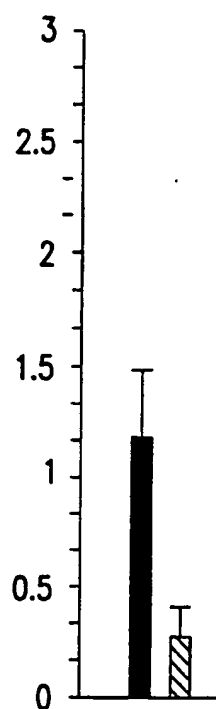


FIG. 25B



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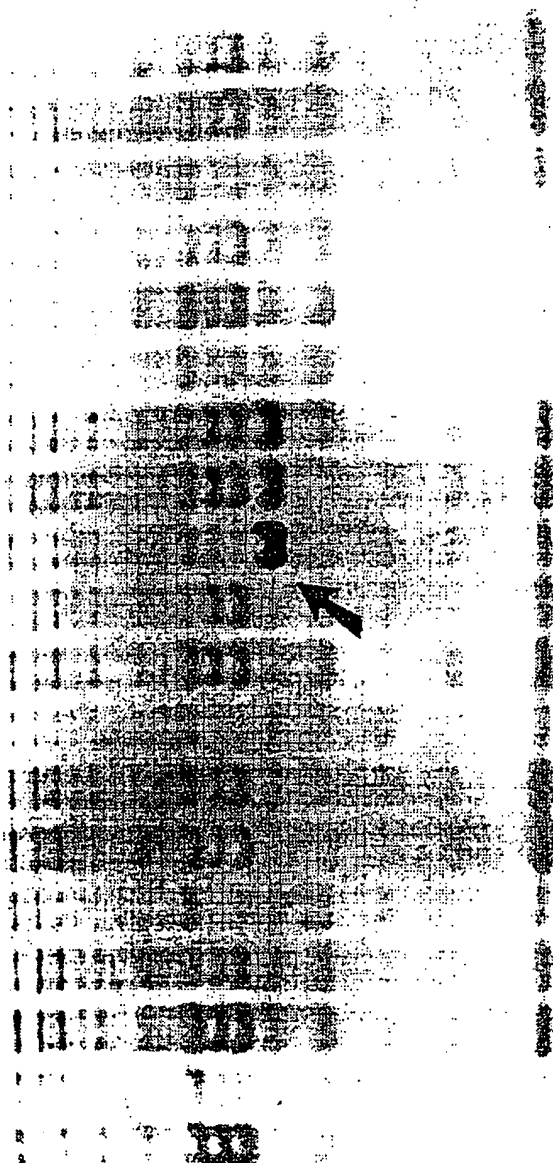


FIG. 26

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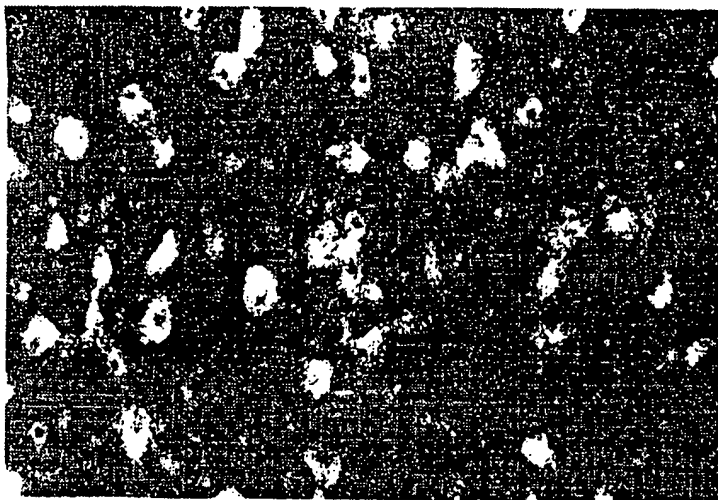


FIG. 27A

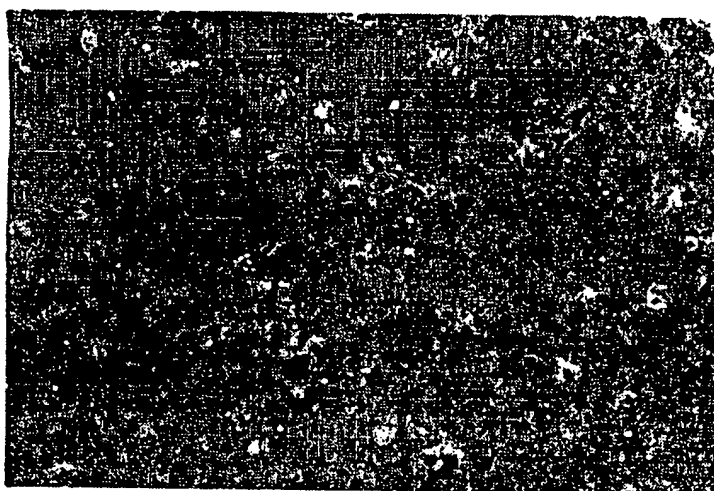


FIG. 27B

SUBSTITUTE SHEET (RULE 26)

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/04321

<b>A. CLASSIFICATION OF SUBJECT MATTER</b> IPC(5) : Please See Extra Sheet. US CL : 424/9; 435/6, 7, 70.5, 240.2, 320.1; 530/350; 536/23.5, 24.5; 514/44 According to International Patent Classification (IPC) or to both national classification and IPC																				
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) U.S. : 424/9; 435/6, 7, 70.5, 240.2, 320.1; 530/350; 536/23.5, 24.5; 514/44 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)																				
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>																				
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.																		
Y	Nature, Volume 341, issued 21 September 1989, C.L. Joachim et al, "Amyloid $\beta$ -Protein Deposits in Tissues Other Than Brain in Alzheimer's Disease", pages 226-230, especially page 226-227 figure 1.	1-39																		
Y	Science, Volume 248, issued 18 May 1990, S. A. Johnson et al, "Relation of Neuronal APP751/APP-695 mRNA Ratio and Neuritic Plaque Density in Alzheimer's Disease", pages 854-857, especially page 856 figure 2.	51-52 and 93																		
Y	Lancet, Volume 339, issued 21 March 1992, A. A. Gutierrez et al, "Gene Therapy for Cancer", pages 715-721, especially page 717, col. 1, parag. 2 to col. 2, through parag. 2 and page 719, parag. 2 to page 720, through parag. 2.	73-89 and 92																		
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.																				
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"E" earlier document published on or after the international filing date	Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art																		
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Date of the actual completion of the international search 14 JULY 1994		Date of mailing of the international search report 27 JUL 1994																		
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer: Deborah Crouch <i>A. Kuyba for</i> Telephone No. (703) 308-0196																		

## INTERNATIONAL SEARCH REPORT

1 national application No.  
PCT/US94/04321

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, A, 90/06993 (WANDS ET AL) 28 June 1990, page 7, line 23 to page 8, line 30, page 47, line 10 to page 55, line 35, page 57, line 5 to page 58, line 24 and page 59, line 25 to page 61, line 21.	1-72, 90,91 and 93

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/04321

## A. CLASSIFICATION OF SUBJECT MATTER: IPC (5):

A61K 49/00,31/70; C12Q 1/68,1/00,C12N 5/00,15/00; C12P 21/02; C07K 3/00; C07H 15/12

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